

78622

STIC-Biotech/ChemLib

From: Davis, Minh-Tam
Sent: Thursday, October 24, 2002 12:45 PM
To: STIC-Biotech/ChemLib
Subject: Search request for 09/807200

Please search in commercial data base and in issued patent files:

SEQ ID NO:1

Thank you.

MINH TAM DAVIS

ART UNIT 1642, ROOM 8A01, MB 8E12

305-2008

CRFE

Point of Contact
P. Sheppard
Telephone number: (703) 308-4499

10/31/02

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2002, 06:21:57 ; Search time 1987 Seconds
(without alignments)
12498.439 Million cell updates/sec

Title: US-09-807-200-1

Perfect score: 1840

Sequence: 1 ctcgagccgggtggcgag.....ctgttgctcaaaaaaaaaa 1840

Scoring table: IDENTITY_NUC

Gapop 10.0 , Capext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

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2: em_esthum:*
3: em_estnu:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_estl:*
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11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	990.8	53.8	1025	9	AL574221
2	981.2	53.3	1009	9	AL554923
3	949.6	51.6	963	9	AL546511
C 4	924	50.2	989	9	AL564981
5	909	49.4	971	9	AL550317
C 6	899	48.9	1011	9	AL574979
C 7	893.4	48.6	981	9	AL575679
C 8	891.6	48.5	950	9	AL577524
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10	870	47.3	934	9	AL552365
11	838.8	45.6	904	9	AL551401
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13	832.2	45.2	843	10	BG741018
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ALIGNMENTS

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LOCUS AL574221 LTI_NFL006_PL2 1025 bp mRNA linear EST 16-FEB-2001
DEFINITION prime. mRNA sequence.

ACCESSION AL574221

VERSION AL574221.1 GI:12934220

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 Evry cedex - France

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

Location/Qualifiers

1. .1025

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/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CS0D1039YK16"

/clone_lib="LTI_NFL006_PL2"

/tissue_type="placenta"

/note="Vector: pCMVSPORT 6; Site.1: NotI; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-stranded cDNA was digested with Not I and

cloned into the Not I and Eco RV sites of the pCMVSPORT 6

vector. Library was normalized. Library was constructed by

Life Technologies. Contact : Feng Liang Life Technologies,

a division of Invitrogen 9800 Medical Center Drive

Rockville, Maryland 20850, USA Fax : (1) 301 610 8371

Email : fliang@life.com URL :

http://fulllength.invitrogen.com"

192 a 306 c 343 g 176 t

8 others

BASE COUNT

ORIGIN

Query Match		53.8%;	Score 990.8;	DB 9;	Length 1025;
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Qy	897	CCAACTTCCACATCCCGACGACACGCTGACCGAGATAACGTCTCTCTCCAGCC	956		
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Qy	957	ACCGGCCAACTCCTTCTACTACCCGGCTGAAGGCCCTGCCTCCATCGCCAGGGTGA	1016		
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Qy	1137	TCCTCCCTGTGCTGCTGGGACTGTGCGAGGCCACTGTGGAGGCTCGGGACCAAGA	1196		
- Db	665	TCCTCCCTGTGCTGCTGGGACTGTGCGAGGCCACTGTGGAGGCTCGGGACCAAGA	606		
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AL554923

LOCUS
DEFINITION

AL554923 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI087YL11 5
prime, mRNA sequence.

ACCESSION
AL554923

VERSION
AL554923.1

KEYWORDS
EST.

SOURCE
human.

ORGANISM
Homo sapiens

REFERENCE
1 (bases 1 to 1009)

AUTHORS
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE
Full-length cDNA libraries and normalization

JOURNAL
Unpublished (2001)

COMMENT
Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

Location/Qualifiers

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/clone="CS0DI087YL11"

/tissue_type="placenta"

/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-stranded cDNA was digested with Not I and

cloned into the Not I and Eco RV sites of the pCMVSPORT 6

vector. Library was normalized. Library was constructed by

Life Technologies. Contact : Feng Liang Life Technologies,

a division of Invitrogen 9800 Medical Center Drive

Rockville, Maryland 20850, USA Fax : (1) 301 610 8371

Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com"

BASE COUNT 155 a 360 c 326 g 157 t 11 others

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Query Match 53.3%; Score 981.2; DB 9; Length 1009;

Best Local Similarity 98.2%; Pred. No. 5 6e-150;

Matches 991; Conservative 8; Mismatches 9; Indels 1; Gaps 1;

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Db 61 CGGGCTTAATAGAGCTCCGGGCTCTGGCTGGGACCCGACCGCTGCCGCGCGCTCCC 120

Qy 282 GCTGCTCTCTCCGGGTGATGGAACCCAGCCGCGCGCGCGCTTGCGGAAGCCCTCT 341

Db 121 GCTGCTCTCTCCGGGTGATGGAACCCAGCCGCGCGCGCTTGCGGAAGCCCTCT 180

Qy 342 GCCT 401

Db 181 GCCT 240

Qy 402 GTTCCGCGAGAGCCCGCGGCAATACAGCATCACCITTCAGGGCAAGTGAGCCAGCG 461

Db 241 GTWCCGCGAGAGCCCGCGGCAATACAGCATCACCITTCAGGGCAAGTGAGCCAGCG 300

Qy 462 CCTTCCCAGAGAGTACCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 521

Db 301 CCTTCCCAGAGAGTACCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360

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VERSION AL546511.1 GI:12879698
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 963)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
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enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 153 a 345 c 312 g 151 t 2 others
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Query Match 51.6%; Score 949.6; DB 9; Length 963;
Best Local Similarity 99.6%; Pred. No. 7.6e-145;
Matches 960; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
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Db 601 GCTTACCTTCTCTCTCCCGCAACTTCGCCACATCCGCGAGCACACGCTGACCGAGATAA 660
Qy 939 CGTCTCTCTCTCCAGCACCGCGCCAACTCTTCTACTACCCCGGCTGAAGGCCCTGC 998
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Qy 999 CTCCTTCGCGAGGTGACACTGTGCGGTGCGACAGAGCCCCAGGGCCTTCATCCCTC 1058
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Qy 1119 CGCGCTGGAGTGGAGGTCTCCCTGTGGTGTCTGCGGACTGTGGGAGGCCACTGTG 1178
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```

enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

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Db 841 CGCGCTGGACTGCGAGGTCTCCCTGGTCTCTGGGAGTCTGGGCGG-CACTGTG 899
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DEFINITION prime, mRNA sequence.
ACCESSION AL564981
VERSION AL564981.1 GI:12915901
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 989)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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1. 989
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/note="Vector: pCMVSPORT 6; Site 1: NotI; primer: 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Enriched, double-stranded cDNA was digested with Not I and
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was constructed by Life Technologies.
Contact : Feng Liang Life Technologies, a division of
Invitrogen 9800 Medical Center Drive Rockville, Maryland
20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 196 a 278 c 338 g 154 t 23 others
ORIGIN

Query Match 50.2%; Score 924; DB 9; Length 989;
Best Local Similarity 95.6%; Pred. No. 1.le-140;
Matches 943; Conservative 23; Mismatches 18; Indels 2; Gaps 2;

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Db 626 GTTCCAGAAACGCCGCTGAGTCTCCCTGTGCTGCTGCTGGGACTGTGGCGA 567
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Qy 1229 AACACGGGAGCCCTGCCCGAGCTCAAGAGAGGCTGAGTGGTCCCTGATAACTGC 1288
Db 506 AACACGGGAGCCCTGCCCGAGCTCGAAGAGAGGCTGAGTGGTCCCTGATAACTGC 447
Qy 1289 GTCTAAGACACAGAGCCCGAGCCCTGGGCGCCCGAGCCATGGGCTGTGCGGGCT 1348
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Db 146 TTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 87
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DEFINITION prime, mRNA sequence.
ACCESSION AL550317
VERSION AL550317.1 GI:12887174
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 971)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers

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was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 147 a 354 c 315 g 152 t 3 others
ORIGIN

Query Match 49.4%; Score 909; DB 9; Length 971;
Best Local Similarity 99.08; Pred. No. 3e-138;
Matches 964; Conservative 2; Mismatches 3; Indels 5; Gaps 5;

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Qy 226 CTTAATAGGAGCTCCGGCTCTGGCTGGGACCCGACCGCTGCCGGCGCGCTCCGCTG 285
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Qy 286 CTCCTGCGGGTGATGGAACACCCAGCCGCGCGCGCGCGCTGGCAAGGCCCTCTGCGC 345
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Qy 406 CGCCAGAGCCCGGCAATACAGCATCACCTTCACGGGCAAGTGGAGCCAGCGCCTT 465
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Qy 466 CCCAAGCAGTACCCCTGTTCGCCGCCCTCGCGCAGTGTCTTCGCTGTGGGGCGCGC 525
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ACCESSION AL574979
VERSION AL574979.1 GI:12935698
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li W.B., Gruber C., Jessee J. and Polayes D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 189 a 295 c 343 g 174 t 10 others
ORIGIN

Query Match 48.9%; Score 899; DB 9; Length 1011;
Best Local Similarity 96.5%; Pred. No. 1.3e-136;
Matches 951; Conservative 8; Mismatches 21; Indels 5; Gaps 4;

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Q	y	1637	TCCAGGGCCCTGGCTCCACGCTGGTTGCAGATACCTCAGACCTGGTGTCTAGGCTGTGC	1696
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Q	y	1697	TGAGGCCACTCTCCGAGGGCGCATCCAAAGCGGGGCCACTTGAGAAGTGAATAAATGGG	1756
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LOCUS	AL575679
DEFINITION	LT1_NFL006_PL2 Homo sapiens cDNA clone CS0DI069YF21 3 prime, mRNA sequence.
ACCESSION	AL575679
VERSION	AL575679.1 GI:12937078
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 981) Li.W.B., Gruber.C., Jesse,J. and Polaves.D.
REFERENCE	
AUTHORS	Jesse,J. and Polaves,D.

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ACCESSION AL577524
VERSION AL577524.1 GI:12940739
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 950)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191*91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

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was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 169 a 267 c 327 g 160 t 27 others
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Query Match 48.5%; Score 891.6; DB 9; Length 950;
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RESULT 9
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ACCESSION AL532820
VERSION AL532820.1 GI:12796313
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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DEFINITION	AL551401	prime, mRNA sequence.	clone CS0D1064YC22 5
ACCESSION	AL551401		
VERSION	AL551401.1	GI:12889312	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 904)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source

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/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 145 a 319 c 289 g 148 t 3 others
ORIGIN

Query Match 45.6%; Score 838.8; DB 9; Length 904;
Best Local Similarity 98.6%; Pred. No. 7.5e-127;
Matches 895; Conservative 3; Mismatches 5; Indels 5; Gaps 5;

QY 287 TCCTGCGGCTGATGAAACCCACCGCGCGCGCCCTGGGCAAGGCCCTCTCGCT 346
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QY 467 CCCAAGCAGTACCCCTGTTCGCCGCCCTGCGCAAGTGTCTTCGCTGTGGGGCGCG 526
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QY 527 CATAGCTCCGACTACAGCATGTGGAGAAACACAGTACGTACGTACAGGCTGCGCGAC 586
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QY 587 TTTGCGAGCGCGCGCGCGCGCTGGGCGCTGATGAAGAGATCGAGCGCGGGGAGCG 646
Db 301 TTTGCGGA- SGCGCGCAGGCTGGGCGCTGATGAAGAGATCGAGCGCGGGGAGCG 359

QY 647 CTGCAGAGCGTGCACAGGTGTTTCGGCGCGCGCGCTCCCGAGCGCGCGGAGACG 706
Db 360 CTGCAGAGCGTGCACAGGTGTTTCGGCGCGCGCGCTCCCGAGCGCGCGGAGACG 419

QY 707 TCGCGGAGCTGGAGTGCAGCGCAGGCACTCGCTGCTCTGCTGCTGCTGCTGCTGCTG 766
Db 420 TCGCGGA- CTGAGGTGCAGCGCAGGCACTCGCTGCTCTGCTGCTGCTGCTGCTGCTG 478

QY 767 CCCAGCCCGACTGTTCTGTTGGGCGTGGAGAGCTGCGAGCTGTGCGACGGGACCTTGG 826
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QY 827 CGGGAACAGCGCGCTGAGACCTGTACCCCTAGACCGCGGAGCGAGCGGCTTCAAC 886
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QY 1126 GGAATCGGAGGCTCCCTGTGTCGTCGCGGACACTGCGGAGGCACTGTGGAGGCT 1185
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Db 838 GGAATCGGAGGCTCCCTGTGTCGTCGCGGACACTGTGCGGA-GSACTGTGGAGGCT 896
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QY 1186 CGGGACCA 1193
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VERSION AL577445.1 GI:12940581
KEYWORDS EST.
SOURCE human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 854)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 168 a 248 c 288 g 145 t 5 others
ORIGIN

Query Match 45.4%; Score 836.2; DB 9; Length 854;
Best Local similarity 98.9%; Pred. No. 2e-126;
Matches 838; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 935 ATAAAGTCTCTCTCCAGCACCAGCGCAACTCTTCTACTACCGCGGCTGAAGGCC 994
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COMMENT

Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10637 row: j column: 11
High quality sequence stop: 823.

FEATURES

source

Location/Qualifiers

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/clone="IMAGE:4779754"

/clone_lib="NCL_CGAP_Skn3"

/lab_host="DH10B (T1 phage-resistant)"

/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.5kb. Library constructed by Life

Technologies. Note: this is a NCL_CGAP Library."

140 a 304 c 238 g 161 t

BASE COUNT

ORIGIN

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Best Local Similarity 99.6%; Pred. No. 8.8e-126;

Matches 834; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 926 GTGACCCAGATACGTCCTCTCTCCAGCCACCCGCCCAACTCTCTACTACCCCGCG 985

Db 61 GTGACCCAGATACGTCCTCTCTCCAGCCACCCGCCCAACTCTCTACTACCCCGCG 120

QY 986 CTGAAGGCCCTCCCTCCCATCGCAGGGTGACACTGTGGGCTGCGACAGAGAGCCCGCAGG 1045

Db 121 CTGAAGGCCCTCCCTCCCATCGCAGGGTGACACTGTGGGCTGCGACAGAGAGCCCGCAGG 180

QY 1046 GCCTTCATCCCTCCGCCCGCAGTCTCCGCCAGGAGCAATGAGATTGACAGCGCC 1105

Db 181 GCCTTCATCCCTCCGCCCGCAGTCTCCGCCAGGAGCAATGAGATTGACAGCGCC 240

QY 1106 TCAGTTCCAGAAAGCGCGTGGACTGGAGTCTCCCTGTGGTCTCTGGGACCTGTC 1165

Db 241 TCAGTTCCAGAAAGCGCGTGGACTGGAGTCTCCCTGTGGTCTCTGGGACCTGTC 300

QY 1166 GGAGGCCACTGTGGAGGCTCGGACCAAGAGGAGTCTGCTACGTCCGGGTCCAGCCC 1225

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QY 1226 GCCAACACGGAGCCCTCGCCCGAGCTCGAAGAGAGGCTGAGTCGCTCCCTGATAAC 1285

Db 361 GCCAACACGGAGCCCTCGCCCGAGCTCGAAGAGAGGCTGAGTCGCTCCCTGATAAC 420

QY 1286 TGGCTCTAAGACCAGAGCCCGAGCCCTTGGGGCCCCCGGACCCATGGGGTGTGCGGG 1345

Db 421 TGGCTCTAAGACCAGAGCCCGAGCCCTTGGGGCCCCCGGAGCCATGGGGTGTGCGGG 480

QY 1346 GCTCCTGTGAGGCTCATGTGACAGGGCGCGAGGGCACAGGGGTTCGCGCTGTCCT 1405

Db 481 GCTCCTGTGAGGCTCATGTGACAGGGCGCGAGGGCACAGGGGTTCGCGCTGTCCT 540

QY 1406 GACCGCGTGAGCGCGCGGACCATCTCTGCACTGAAGGCCCTCTGTTGGCGGCGACG 1465

Db 541 GACCGCGTGAGCGCGCGGACCATCTCTGCACTGAAGGCCCTCTGTTGGCGGCGACG 600

QY 1466 GCAATGGGAAACAGCCCTCTCTCCCAACCTTCTTAGGGGCCCGCGTGTCCCG 1525

Db 601 GCAATGGGAAACAGCCCTCTCTCCCAACCTTCTTAGGGGCCCGCGTGTCCCG 660

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Db 661 TCTGCTCTCAGCCTCCTA 720
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Db 721 AATTATGCTCTCTTATAAGTTATTGCTCTCCAGGAGATTGCTTTCATCGTCCAGGGC 780
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QY 1646 CTGGCTCCCAAGCGGTTGACAGATACCTTCAGACCTGGTGTCTAGGCTGTCTGAGCC 1702
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Db 781 CTGGCTCCCAAGCGGTTGACAGATACCTTCAGACCTGGTGTCTAGGCTGTCTGAGCC 837

RESULT 14

AL551786

LOCUS

DEFINITION

AL551786 LTI_NFL006_PL2

prime, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1..979

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/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA

was primed with a NotI-oligo(dt) primer. Five prime end

enriched, double-stranded cDNA was digested with Not I and

cloned into the Not I and Eco RV sites of the pCMVSPORT 6

vector. Library was normalized. Library was constructed by

Life Technologies. Contact: Feng Liang Life Technologies,

a division of Invitrogen 9800 Medical Center Drive

Rockville, Maryland 20850, USA Fax: (1) 301 610 8371

Email: fliang@lifetech.com URL:

http://fulllength.invitrogen.com"

BASE COUNT

ORIGIN

166 a 334 c 307 g 156 t 16 others

Query Match 45.2%; Score 831.6; DB 9; Length 979;

Best Local Similarity 95.8%; Pred. No. 1.1e-125;

Matches 944; Conservative 11; Mismatches 20; Indels 10; Gaps 10;

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QY 374 GGCAGGCTCTTGGGGGAGAGTCCATCTGTCGCCAGAGCCCGGGCAATACAGCATC 433

Db 61 GGCAGGCTCTTGGGGGAGAGTCCATCTGTCGCCAGAGCCCGGGCAATACAGCATC 120

QY 434 ACCTTCACGGGCAAGTGGAGCCAGACGGCCTTCCCAAGCAGTACCCCTGTTCCGCCCC 493

Db 121 ACCTTCACGGGCAAGTGGAGCCAGACGGCCTTCCCAAGCAGTACCCCTGTTCCGCCCC 180

QY 494 CTTGCGCAGTGGTCTTCGCTGTGGGGCGCGCATAGCTCCGACTACAGCATGTGGAGG 553

Db 181 CTTGCGCAGTGGTCTTCGCTGTGGGGCGCGCATAGCTCCGACTACAGCATGTGGAGG 240


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Db 719 TGTGTCGCGATCGTGCCAGCCGACTGGTTCTGTCGGCGTGACAGCCTGGACCTGTG 778
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Search completed: October 27, 2002, 11:14:29
Job time : 2003 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2002, 06:19:17 ; Search time 3403 Seconds

(without alignments)
11314.965 Million cell updates/sec

Title: US-09-807-200-1

Perfect score: 1840

Sequence: 1 ctcgagcggggtgcgcag.....ctgtgtctcaaaaaaaaaa 1840

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: gb_hgt:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vi:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_on:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vi:*

30: em_hgt_hum:*

31: em_hgt_inv:*

32: em_hgt_other:*

33: em_hgtgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1761.2	95.7	1785	6	AX203883	AX203883 Sequence
3	1692.4	92.0	1779	6	AR167936	AR167936 Sequence
4	1599.4	86.9	1634	9	BC002707	BC002707 Homo sapi
5	1100.2	59.8	1105	6	AR035961	AR035961 Sequence
6	988	53.7	996	6	BD006592	BD006592 Integrin
7	729.2	39.6	2820	9	AK026054	AK026054 Homo sapi
8	726.4	39.5	190462	9	AC092535	AC092535 Homo sapi
9	726.4	39.5	197176	2	AC022763	AC022763 Homo sapi
10	724	39.3	4292	9	AK024499	AK024499 Homo sapi
11	685.8	37.3	2325	10	AF155196	AF155196 Rattus no
12	679	36.9	1778	10	BC017616	BC017616 Mus muscu
13	549.8	29.9	1020	6	BD006593	BD006593 Integrin
14	364.2	19.8	2116	5	AB006085	AB006085 Danio rer
15	343.8	18.7	400	6	AR037874	AR037874 Sequence
16	339	18.4	400	6	AR125230	AR125230 Sequence
17	304.8	16.6	506	6	AR035966	AR035966 Sequence
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19	259.6	14.1	3381	5	AB006084	AB006084 Danio rer
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21	204.2	11.1	316	6	AR035968	AR035968 Sequence
22	119.8	6.5	2565	3	DMAF000178	AF000178 Drosophill
23	110.6	6.0	3489	3	BFL6096	AJ06096 Branchios
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27	81.6	4.4	2836	3	AY058267	AY058267 Drosophill
28	81.2	4.4	3146	5	AB006086	AB006086 Danio rer
29	79.6	4.3	4061	6	AB051389	AB051389 Bos tauru
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31	77.8	4.2	51289	3	AC005717	AC005717 Drosophill
32	77.8	4.2	73721	2	AC020007	AC020007 Drosophill
33	77.8	4.2	163072	3	AC099032	AC099032 Drosophill
34	77.8	4.2	259817	3	AE003804	AE003804 Drosophill
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44	71.6	3.9	4035	10	BC020531	BC020531 Mus muscu
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ALIGNMENTS

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ACCESSION	AB027466.1	GI:6172220				
VERSION	SPON2; spondin 2.					
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SOURCE	Homo sapiens					
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1 (sites)					
AUTHORS	Manda, R., Kohno, T., Matsuno, Y., Takenoshita, S., Kuwano, H. and Yokota, J.					
TITLE	Identification of genes (SPON2 and c20orf2) differentially expressed between cancerous and noncancerous lung cells by mRNA differential display					
JOURNAL	Genomics 61 (1), 5-14 (1999)					
MEDLINE	99443867					
REFERENCE	2 (bases 1 to 1807)					
AUTHORS	Yokota, J., Kohno, T. and Manda, R.					
TITLE	Direct Submission					
JOURNAL	Submitted (18-MAY-1999) Jun Yokota, National Cancer Center Research					

Institute, Biology Division; Tsukiji 5-chome 1-1, Chuo-ku, Tokyo
104-0045, Japan (E-mail: j yokota@an2.ncc.go.jp, Tel: 81-3-3547-5272,
Fax: 81-3-3542-0807)

FEATURES
Source

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ORIGIN

Query Match 95.9%; Score 1764.4; DB 9; Length 1807;
Best Local Similarity 99.8%; Pred. No. 2.3e-249;
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ACCESSION	AX203883		linear
VERSION	AX203883.1	GI:15393341	PAT 30-AUG-2001
KEYWORDS	human.		
SOURCE			
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 1785)		
JOURNAL	Harkins,R., Parkes,D., Parry,G., Schneider,D.W. and Steinbrecher,R.		
FEATURES	Dna encoding a novel rgl polypeptide		
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QY	129	CAGTCTCTATCTCGCTTCGCTTGAGGCCAGGGCGTGCAGCATCGAGACAGGAGCACT	188
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RESULT 4
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LOCUS
DEFINITION
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ACCESSION
  BC002707
VERSION
  BC002707.1 GI:12803740
KEYWORDS
  MGC.
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 1634)
  Direct Submission
  Submitted (05-FEB-2001) National Institutes of Health, Mammalian
  Gene Collection (MGC), Cancer Genomics Office, National Cancer
  Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
  USA
  NIH-MGC Project URL: http://mgc.nci.nih.gov
  Contact: MGC help desk
  Email: cgapbs@mail.nih.gov
  Tissue Procurement: ATCC
  cDNA Library Preparation: Rubin Laboratory
  DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  Sequencing Center (NISC),
  Gaithersburg, Maryland.
  Web site: http://www.nisc.nih.gov/
  Contact: nisc.mgc@nih.gov
  Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
  Shevchenko, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
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  Lim, M., Maduro, O.L., Masiello, C., Mastrian, S.D., McCloskey, J.C.,
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  Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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This clone was selected for full length sequencing because it
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FEATURES
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 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
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 ORGANISM
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 AUTHORS
 TITLE
 JOURNAL
 FEATURES
 source

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 Sequence 1 from patent US 5871969.
 AR035961
 AR035961.1 GI:5952629
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 Unclassified.
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DEFINITION BD006592
ACCESSION BD006592
VERSION BD006592.1 GI:18634963
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 996)
AUTHORS Jonak,Z.L., Trullis,S.H., Tsui,P. and Lane,P.A.
TITLE Integrin ligand, human Mindin
JOURNAL Patent: JP 2001500386-A 1 16-JAN-2001;
SMITHKLINE BEECHAM CORP
COMMENT OS Homo sapiens (human)
PN JP 2001500386-A/1
PD 16-JAN-2001
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PR 09-MAY-1997 US 60/046106
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RESULT 7

AK026054

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

AK026054 2820 bp mRNA linear PRI 29-SEP-2000
Homo sapiens cDNA: FLJ22401 fis, clone HRC08032, highly similar to
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AK026054 1 GI:10438772
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (sites)

Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y.,
Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
NEDO human cDNA sequencing project
Unpublished (2000)

2 (bases 1 to 2820)
Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,
Shibahara,T., Tanaka,T. and Nakamura,Y.
Direct Submission

Submitted (29-AUG-2000) to the DDBJ/EMBL/GenBank databases. Sumio
Sugano, Institute of Medical Science, University of Tokyo,
Laboratory of Genome Structure Analysis, Human Genome Center;

Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
(E-mail:cdna1@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)

COMMENT NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing: Department of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).

FEATURES

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BASE COUNT

ORIGIN

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DEFINITION Homo sapiens BAC clone RP11-20120 from 4, complete sequence.
ACCESSION AC092535
VERSION AC092535.4 GI:18640695
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
99063792
REFERENCE 2 (bases 1 to 190462)
AUTHORS McLellan, M., Cotton, M. and Dixon, R.
TITLE The sequence of Homo sapiens BAC clone RP11-20120
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 190462)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 190462)
Waterston, R.
Direct Submission
Submitted (08-FEB-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Feb 8, 2002 this sequence version replaced gi:15825624.

Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu

Summary Statistics

Center project name: H_NH0020120

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frenken, E., Tatenoh, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome

libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)
 VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-460119; the clone sequenced to the right is RP11-386115. Actual start of this clone is at base position 1 of RP11-20120; actual end is at base position 190462 of RP11-20120.

Data from AC078852 was used to finish this clone, AC092535.

Polymorphisms have been identified between AC078852 and AC092535. Single subclone region exists between 13867 and 13921. There is an unresolved tandem repeat from base 172834 to 175299.

FEATURES

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DEFINITION Homo sapiens clone RP11-296G16, WORKING DRAFT SEQUENCE, 24
unordered pieces.
AC022763
AC022763.2 GI:7652738
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS human.
SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 197176)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens, clone RP11-296G16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 197176)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F.,
Bozulavkiy,L., Boukhgalter,B., Brown,A., Burkett,G., Castle,A.,
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Landers,T., Lehoczy,J., Levine,R., Liu,C., Liu,G., Locke,K.,
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Norman,C.H., O'Connor,T., O'Donnell,P., Olivari,T.M., Peterson,K.,
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Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
Zimmer,A. and Zody,M.
Direct Submission
Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Apr 27, 2000 this sequence version replaced gi:6987625.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L5843
Center clone name: 296_G-16
----- Summary Statistics
Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 185565 bases at least Q40
Consensus quality: 190999 bases at least Q30
Consensus quality: 192979 bases at least Q20
Insert size: 188000; agarose-fp
Insert size: 194876; sum-of-contigs
Quality coverage: 4.5 in Q20 bases; agarose-fp
Quality coverage: 4.4 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 24 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 539 2494: contig of 1956 bp in length
* 2495 2594: gap of 100 bp
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* 3741 3840: gap of 100 bp
* 3841 6181: contig of 2341 bp in length
* 6182 6281: gap of 100 bp
* 6282 8921: contig of 2640 bp in length
* 8922 9021: gap of 100 bp
* 9022 12132: contig of 3111 bp in length
* 12133 12232: gap of 100 bp
* 12233 15557: contig of 3325 bp in length
* 15558 15657: gap of 100 bp
* 15658 19986: contig of 4329 bp in length
* 19987 20086: gap of 100 bp
* 20087 21983: contig of 1897 bp in length
* 21984 22083: gap of 100 bp
* 22084 26850: contig of 4767 bp in length
* 26851 26950: gap of 100 bp
* 26951 33137: contig of 4367 bp in length
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* 36114 41819: contig of 5706 bp in length
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TITLE
JOURNAL
COMMENT

* 46145 52849: contig of 6705 bp in length
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* 105064 105163: gap of 100 bp
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FEATURES

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Best Local Similarity 99.9%; Pred. No. 9.3e-98;
Matches 727; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 10
AK024499

LOCUS

AK024499 Homo sapiens mRNA for FLJ00108 protein, partial cds.
DEFINITION

AK024499

ACCESSION

AK024499.1 GI:10440517

VERSION

keywords

DESCRIPTION

ORGANISM

Source

Organism

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4292)
AUTHORS Ohara, O., Nagase, T., Kikuno, R. and Okumura, K.
TITLE The nucleotide sequence of a long cDNA clone isolated from human spleen

JOURNAL Published Only in DataBase (2000) In press

REFERENCE 2 (bases 1 to 4292)

AUTHORS Ohara, O., Nagase, T., Kikuno, R. and Okumura, K.

JOURNAL Submitted (24-AUG-2000) Osamu Ohara, Kazusa DNA Research Institute,

Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
URL: <http://www.kazusa.or.jp/NEDO>, Tel: 81-438-52-3913,
Fax: 81-438-52-3914)

COMMENT NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection; Kazusa DNA Research Institute.

FEATURES Location/Qualifiers

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/dev_stage="adult"

/note="vector:pBluescriptII SK plus"

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CDS <1..653

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/protein_id="BAB15789.1"

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BASE COUNT 788 a 1323 c 1349 g 832 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 4.7e-97;

Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3568 CAGTTCAGAAAGCGCTGGACTGGAGGTCTCCCTGTGGTCTCTGGGACTGTGG 3627

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QY 1167 GAGGCACATCTGGAGGCTCGGACCAAGCAGGAGTCTGCTACGTCGCGGTCCAGCCCG 1226

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Db 3808 CTCCTGTGAGGCTCATGTGTCAGGGCGCGGAGGGCACAGGGGGTTTCGCGTCTCTTG 3867

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QY 1407 ACCGCGGTGAGGCGCGGACCAATCTCTGCACTGAAGGGCCCTCTGTTGGCGGCACGG 1466

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Db 4108 TGGCTCTCCACGCTGTCAGATACCTCAGACCTGTCGCTAGGCTGTCGAGCCACT 4167

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Db 4288 CTCGA 4291

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RESULT 11

AF155196 2325 bp mRNA linear ROD 23-DEC-1999

LOCUS Rattus norvegicus mindin precursor, mRNA, complete cds.

DEFINITION AF155196

ACCESSION AF155196

VERSION AF155196.1 GI:5031505

KEYWORDS Norway rat.

SOURCE Rattus norvegicus

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

REFERENCE 1 (bases 1 to 2325)

AUTHORS Feinstein, Y., Borrell, V., Garcia, C., Burstyn-Cohen, T., Tzarfaty, V.,

Franklin, A., Nose, A., Okamoto, H., Higashijima, S., Soriano, A. and

Klar, A.

FEAT

F-spondin and mindin: two structurally and functionally related

genes expressed in the hippocampus that promote outgrowth of

embryonic hippocampal neurons

Development 126 (16), 3637-3648 (1999)

JOURNAL 99339921

MEDLINE 10409509

PUBMED 2 (bases 1 to 2325)

REFERENCE Feinstein, Y., Borrell, V., Garcia, C., Burstyn-Cohen, T., Tzarfaty, V.,

Franklin, A., Nose, A., Okamoto, H., Higashijima, S., Soriano, A. and

Klar, A.

Direct Submission

Submitted (30-JAN-1999) Anatomy & Cell Biology, Hebrew University,

PO Box 12272, Jerusalem 91120, Israel

Location/Qualifiers

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/strain="Sprague Dawley"

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CDS


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410 a 503 c 486 g 379 t
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Best Local Similarity 75.5%; Pred. No. 2.2e-90;
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QY 154 GCGCAGGCGCTGAGCATGGAAGCAGGAGAACTGGAGCTCATTTGGCGCGCCGGGGC 213
DB 78 GACCAGGCACTGAGGCA--GAAGACAGGAGAGCTGGGGCT-ATCTGCTGGCCAGAGG 134
QY 214 GCGCGGCTCGGCTTAAATAGGAGCTCCGGCTCTGGCTGGGACCGACGCTGCGCGCC 273
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QY 274 GC-----GCCTCGCGCTCTCTCGCGGGTGATGAAACCCAGCCGCGCGCGCC 325
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QY 383 CTGTTGGGGAGAGTCCATCTGTTCCGCGCAGAGCCCGGCCAAATACAGCATCAGCTTCACG 442
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DB 369 GGCAAGTGGAGCCAGCAGCATTTCCCAAGCAGTACCCCTGTTCGCGCCCGCTGCGCAG 428
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DB 429 TGTCTCTCTGCTGCGGGGCGAGTCAAGCTCTGACTACAGCATGTGGGGGAAGATGAG 488
QY 563 TAGCTCAGTAACGCGCTGCGGACTTTGGGAGCGCGGCGAGCGCTGGGCGCTGATGAG 622
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QY 983 CGGCTGAAGGCGCTGCTCCCTCCGACGAGGTGACACTGCTGCGCTGGGACAGAGCCCC 1042
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DB 1209 AACTGCTCTAAGACGAGACTCCAGTAGC 1237
RESULT 13
BD006593
LOCUS Integrin ligand, human Mindin.
DEFINITION BD006593
ACCESSION BD006593.1 GI:18634964
VERSION JP 2001500386-A/2.
KEYWORDS Homo sapiens.
SOURCE Homo sapiens.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE 1 (bases 1 to 1020)
AUTHORS Jonak,Z.L., Trullis,S.H., Tsui,P. and Lane,P.A.
TITLE Integrin ligand, human Mindin
JOURNAL Patent: JP 2001500386-A 2 16-JAN-2001;
SMITHKLINE BEECHAM CORP
COMMENT OS Homo sapiens (human)
PN JP 2001500386-A/2
PD 16-JAN-2001
PF 07-MAY-1998 JP 1998548555
PR 09-MAY-1997 US 60/046106
PI ZENKA L JONAK,STEPHEN H TRULLI,PING TSUI,PAMELA A LANE PC
A61K39/395,A61K48/00,C07H21/04,C07K14/435,C07K14/705,C07K16/00, PC
C07K16/28,
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QY 1262 GAGGCTGAGTCGGTCCCTGATACCTAAAGACAGAGCCCGCAGCCCC 1314

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RESULT 15
AR037874
LOCUS
DEFINITION Sequence 1 from patent US 5804382.
ACCESSION AR037874
VERSION AR037874.1 GI:5956591
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 400)
AUTHORS Sytkowski,A.J. and Yang,M.
TITLE Methods for identifying differentially expressed genes and
JOURNAL differences between genomic nucleic acid sequences
FEATURES
    Patent: US 5804382-A 1 08-SEP-1998;
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BASE COUNT 70 a 157 c 110 g 63 t
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Best Local Similarity 97.0%; Pred. No. 3.7e-41;
Matches 393; Conservative 0; Mismatches 7; Indels 5; Gaps 4;

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QY 970 CTCTACTACCCGCGCTGAAGCCCTGCCCTCCCATCGCAGGTGACACTGTGGGCT 1029
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Db 119 CTCTACTACCCGCGCTGAAGGCC --TGCTCCCATCGCAGGTGACACTGTGGGCT 176

QY 1030 GCGACAGAGCCCGAGGCGCTTATCCCTCCCGCCAGTCCTGCCAGCAGGCAATGA 1089
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Db 177 GCGACAGAGCCCGAGGCGCTTATCCCTCCCGCCAGTCCTGCCAGCA -GGACAATGA 235

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Search completed: October 27, 2002, 10:47:17
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2002, 03:39:47 ; Search time 298 Seconds
(without alignments)
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Title: US-09-807-200-1
Perfect score: 1840
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1840	100.0	1840	21	AAZ95034
2	1827.6	99.3	1991	22	AAI58028
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4	1812.8	98.5	1846	20	AAZ34089
5	1812.8	98.5	1847	21	AAC78507
6	1812.8	98.5	1847	21	AAC58630
7	1812.8	98.5	1847	21	AAA49728
8	1793.2	97.5	1798	22	AAK94244
9	1761.2	95.7	1785	22	AAF90566

10	1760.2	95.7	1770	22	AAF90567
11	1692.4	92.0	1779	21	RAD20094
12	1686.2	91.6	1718	21	AAC59794
13	1680.8	91.3	1848	22	AAH31981
14	1666.4	90.6	1669	22	AAK94182
15	1563.4	85.0	1607	19	AAV63241
16	1297.2	70.5	1458	21	AAZ52575
17	1100.2	59.8	1105	20	AAZ02019
18	1098.6	59.7	1105	18	AAZ78360
19	988	53.7	996	20	AAV72537
20	734	39.9	2261	21	AAC59258
21	700.8	38.1	763	22	AAK91675
22	700.8	38.1	763	22	AAK93839
23	684.2	37.2	993	19	AAV63258
24	644.6	35.0	825	22	AAK91827
25	644.6	35.0	825	22	AAK93227
26	547.4	29.8	1021	20	AAV72538
27	483	26.2	534	22	AAK92493
28	343.8	18.7	400	19	AAV53726
29	339	18.4	400	20	AAZ06948
30	304.8	16.6	506	20	AAZ02024
31	301.4	16.4	539	22	AAK87746
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33	233.4	12.7	432	19	AAV63270
34	217.8	11.8	553	19	AAV63268
35	204.2	11.1	316	20	AAZ02026
36	204.2	11.1	316	20	AAZ02025
37	204	11.1	204	21	AAZ95016
38	191	10.4	541	19	AAV63266
39	163.6	8.9	470	19	AAV63267
40	121.4	6.6	2574	23	ABL11611
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43	79.6	4.3	4061	20	AAZ30094
44	77.8	4.2	7273	23	ABL11996
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ALIGNMENTS

RESULT 1
AAZ95034
ID AAZ95034 standard; cDNA; 1840 BP.
XX AAZ95034;
AC AAZ95034;
XX
DT 15-AUG-2000 (first entry)
XX Cancer specific gene Prol08 cDNA useful as prostate cancer marker.
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DE Cancer specific gene; CSG; prostate cancer; diagnosis; monitoring;
KW staging; imaging; metastasis; therapy; human; Prol08; ss.
KW
XX Homo sapiens.
OS
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FH Key
FT CDS
FT 299..1294
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XX WO200023108-A1.
XX
PD 27-APR-2000.
XX
XX 18-OCT-1999; 99WO-US23764.
XX
XX 19-OCT-1998; 98US-0104741.
XX
XX (DIAD-) DIADEXUS LLC.
XX
XX Ali SM, Sun Y, Salceda S, Recipon H, Caferkey R;
XX WPI; 2000-339528/29.
DR

DR P-PSDB; AAY79561.
XX
PT Diagnosing, detecting, staging, monitoring, imaging and treating
PT cancers, especially useful for detecting prostate cancer comprises
PT measuring changes in levels of cancer specific genes in cells, tissues
PT and body fluids
XX
PS Claim 6; Page 28-29; 35pp; English.
XX
XX The present sequence is that of a cancer specific gene (CSG)
CC designated pro108. The CSG was identified using a suppression
CC subtractive hybridization method. It is a diagnostic marker
CC for prostate cancer. In 11 different healthy tissues examined,
CC pro108 mRNA expression was highest in ovary and uterus. Expression
CC in healthy prostate was low. However, overexpression of CSG pro108
CC was observed in 13 of 13 prostate cancer tissues examined. CSGs
CC comprising pro108, its encoded polypeptide (see AAY79561), or an
CC antibody that specifically binds CSG, are used in claimed methods
CC for the diagnosis, detection, staging, monitoring, imaging and
CC treatment of prostate cancer. The new methods provide earlier
CC diagnosis for the presence and metastasis of prostate cancer, and
CC can be used to determine if a cancer has metastasized, or to
CC monitor the progress or stage of the disease when it has not
CC metastasized.
XX
SQ Sequence 1840 BP; 305 A; 628 C; 582 G; 325 T; 0 other;
Query Match 100.0%; Score 1840; DB 21; Length 1840;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1840; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTCGAGCCGGGTGCGGACGACTGCGAGGGAAGAGGTGATCCAGCCGGGAAGTTC 60
DB 1 CTCGAGCCGGGTGCGGACGACTGCGAGGGAAGAGGTGATCCAGCCGGGAAGTTC 60
QY 61 GCTGGCAGGGGAGTGGGAAAGCGGAGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC 120
DB 61 GCTGGCAGGGGAGTGGGAAAGCGGAGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC 120
QY 121 CTTTCTCCACGTCCTATCTGCTCTGCTGCTGAGGCGGCGGCTTAAATAGAGTTC 180
DB 121 CTTTCTCCACGTCCTATCTGCTCTGCTGAGGCGGCGGCTTAAATAGAGTTC 180
QY 181 GAGGAATCGAGCTCATTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
DB 181 GAGGAATCGAGCTCATTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
QY 241 CGGGCTCTGGCTGGGACCGGACCGCTGCCGGCGGCGGCTCCCGTCTCTGCGGGTGTAT 300
DB 241 CGGGCTCTGGCTGGGACCGGACCGCTGCCGGCGGCGGCTCCCGTCTCTGCGGGTGTAT 300
QY 301 GGAAACCCAGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
DB 301 GGAAACCCAGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
QY 361 TCTCGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
DB 361 TCTCGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
QY 421 CAAATACAGCATCACCTTACGGGCAAGTGGAGCCAGAGCGGCTTCCCAAGCAGTACCC 480
DB 421 CAAATACAGCATCACCTTACGGGCAAGTGGAGCCAGAGCGGCTTCCCAAGCAGTACCC 480
QY 481 CTTGTTCCGCGCCCTTCCGAGTGGTCTTCTGCTGGGGGCGGCGGCGGCGGCGGCGG 540
DB 481 CTTGTTCCGCGCCCTTCCGAGTGGTCTTCTGCTGGGGGCGGCGGCGGCGGCGGCGG 540
QY 541 CAGCATGTGGAGGAAGAACAGTACGTACGAGGCGGCTGCGGAGCTTGGCGAGCGCGG 600
DB 541 CAGCATGTGGAGGAAGAACAGTACGTACGAGGCGGCTGCGGAGCTTGGCGAGCGCGG 600
QY 601 CGAGGCGCTGGGCGCTGATGAAGGAGATCGAGGCGGCGGCGGCGGCGGCGGCGGCGG 660
DB 601 CGAGGCGCTGGGCGCTGATGAAGGAGATCGAGGCGGCGGCGGCGGCGGCGGCGGCGG 660

DB 601 CGAGGCGCTGGGCGCTGATGAAGGAGATCGAGGCGGCGGCGGCGGCGGCGGCGGCGG 660
QY 661 CGAGGCTGTTTTCGGGCGCGCGCTGCCAGCGCGACCGGCGAGACGCTCGCGGAGCTGGA 720
DB 661 CGAGGCTGTTTTCGGGCGCGCGCTGCCAGCGCGACCGGCGAGACGCTCGCGGAGCTGGA 720
QY 721 GGTGACGCGCAGGCACTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
DB 721 GGTGACGCGCAGGCACTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
QY 781 GTTGTGGCGGTGGACAGCTGGACCTGTGTCAGCGGGGACCGTGGCGGGAACAGCGCGC 840
DB 781 GTTGTGGCGGTGGACAGCTGGACCTGTGTCAGCGGGGACCGTGGCGGGAACAGCGCGC 840
QY 841 GCTGACCTGTACCCCTACGACGCGGGGACGACAGCGCTTACCTTCTCTCCGCCCAA 900
DB 841 GCTGACCTGTACCCCTACGACGCGGGGACGACAGCGCTTACCTTCTCTCCGCCCAA 900
QY 901 CTTGCGCACCATCCCGCAGGACGAGTACCGAGATAAGCTCTCTCTCCAGCCACC 960
DB 901 CTTGCGCACCATCCCGCAGGACGAGTACCGAGATAAGCTCTCTCTCCAGCCACC 960
QY 961 GGCCTAACTCTTCTACTACCCGCGCTGAAGCCCTGCTCCATCGCCAGGCTGACACT 1020
DB 961 GGCCTAACTCTTCTACTACCCGCGCTGAAGCCCTGCTCCATCGCCAGGCTGACACT 1020
QY 1021 GGTGGCGCTGCGACAGAGCCCGAGGCGCTTATCCCTCCCGCCCGAGTCTGCCAGAG 1080
DB 1021 GGTGGCGCTGCGACAGAGCCCGAGGCGCTTATCCCTCCCGCCCGAGTCTGCCAGAG 1080
QY 1081 GGACATGAGATTGTAGACAGCGCTCAGTTCCAGAAACCGCGCTGGAGTGGAGTCTC 1140
DB 1081 GGACATGAGATTGTAGACAGCGCTCAGTTCCAGAAACCGCGCTGGAGTGGAGTCTC 1140
QY 1141 CTTGTGGTCTGCTGCGGACTGTGCGGAGCGGCTGCTGGAGGCTCGGAGCAAGAGAG 1200
DB 1141 CTTGTGGTCTGCTGCGGACTGTGCGGAGCGGCTGCTGGAGGCTCGGAGCAAGAGAG 1200
QY 1201 GACTCGCTACGTCGCGGCTCCAGCCCGCAACAGGAGCGGCTGCGGCGGCTCGAAGA 1260
DB 1201 GACTCGCTACGTCGCGGCTCCAGCCCGCAACAGGAGCGGCTGCGGCGGCTCGAAGA 1260
QY 1261 AGAGGCTAGTGGCTCCCTGATAACTGCTCTAAGACACGAGCCCGCAGCCCTTGGG 1320
DB 1261 AGAGGCTAGTGGCTCCCTGATAACTGCTCTAAGACACGAGCCCGCAGCCCTTGGG 1320
QY 1321 CCCCAGGACCATGGGCTGTCGGGCGCTCTGTGAGGCTCATGCTGAGGCGGCGGAG 1380
DB 1321 CCCCAGGACCATGGGCTGTCGGGCGCTCTGTGAGGCTCATGCTGAGGCGGCGGAG 1380
QY 1381 GCACAGGGGTTTTCGGCTGCTCTGACCGGCTGAGGCGGCGGCGGCGGCGGCTCTG 1440
DB 1381 GCACAGGGGTTTTCGGCTGCTCTGACCGGCTGAGGCGGCGGCGGCGGCGGCTCTG 1440
QY 1441 GAAGGCGCTCTGTTGGCGGCGGCGGCGGCTTGGGAAACAGGCTCTCTCTTCCCAACCT 1500
DB 1441 GAAGGCGCTCTGTTGGCGGCGGCGGCGGCTTGGGAAACAGGCTCTCTCTTCCCAACCT 1500
QY 1501 GCTTCTTAGGGGCGGCGGCTGTCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
DB 1501 GCTTCTTAGGGGCGGCGGCTGTCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
QY 1561 CATCCCAAGGCTCCAGCTACTTAAATATGCTCTCTTATAGTTATGCTGCTCCAG 1620
DB 1561 CATCCCAAGGCTCCAGCTACTTAAATATGCTCTCTTATAGTTATGCTGCTCCAG 1620
QY 1621 AGATTGCTCTTATGCTCCAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
DB 1621 AGATTGCTCTTATGCTCCAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
QY 1681 GTGCTCTAGGCTGTGTGAGCGGCTCTCCGAGGCGGCTCTCCGAGGCGGCGGCGGCTTGA 1740
DB 1681 GTGCTCTAGGCTGTGTGAGCGGCTCTCCGAGGCGGCTCTCCGAGGCGGCGGCGGCTTGA 1740

QY 1741 GAAGTGAATAAATGGGCGGTTTCGGAAGCGTCAGTGTTCATGTTATGGATCTCTCTG 1800
|||||
Db 1741 GAAGTGAATAAATGGGCGGTTTCGGAAGCGTCAGTGTTCATGTTATGGATCTCTCTG 1800
QY 1801 CGTTTGAATAAAGACATCTCTGTTGCTCAAAAAAAAAA 1840
|||||
Db 1801 CGTTTGAATAAAGACATCTCTGTTGCTCAAAAAAAAAA 1840
RESULT 2
AA158028
ID AA158028 standard; cDNA; 1991 BP.
XX
AC AA158028;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 231.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia; ss.
XX
OS Homo sapiens.
XX
XX WO200153312-A1.
PN
XX 26-JUL-2001.
PD
XX 26-DEC-2000; 2000WO-US34263.
PF
XX 21-JAN-2000; 2000US-0488725.
PR
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
PA (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI: 2001-442253/47.
DR
DR P-PSDB; AAM38872.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
PT
XX
PS Claim 1; SEQ ID NO 231; 10078pp; English.
XX
XX The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed

CC specification.
XX
SQ Sequence 1991 BP; 339 A; 669 C; 620 G; 350 T; 13 other;
Query Match 99.3%; Score 1827.6; DB 22; Length 1991;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1830; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 7 CCGGGGTGGCGCAGCACTGCCAGGGGAAGAGGGTGATCCGACCCGGGGAAGGTCTGGTGG 66
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Db 97 CCGGGGTGGCGCAGCACTGCCAGGGGAAGAGGGTGATCCGACCCGGGGAAGGTCTGGTGG 156
QY 67 CAGGGCGAGTTGGGAAAGCGGACGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC 126
|||||
Db 157 CAGGGCGAGTTGGGAAAGCGGACGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC 216
QY 127 CCCACGTCCTATCTGCTCTGCTGAGGCGCAGGCCGCTGCGAGCATCGAAGACAGGAGGAA 186
Db 217 CCCACGTCCTATCTGCTCTGCTGAGGCGCAGGCCGCTGCGAGCATCGAAGACAGGAGGAA 276
QY 187 CTGGAGCCTCATTTGGCGCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCCT 246
Db 277 CTGGAGCCTCATTTGGCGCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCCT 336
QY 247 CTGGCTGGGACCGGACCGGCTGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC 306
Db 337 CTGGCTGGGACCGGACCGGCTGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC 396
QY 307 CCCAGCCCGCGCGCGCGCGCTGGGCAAGGCCCTCTGCGCTCTCTCTCTCTCTCTCTCTCTCG 366
Db 397 CCCAGCCCGCGCGCGCGCGCTGGGCAAGGCCCTCTGCGCTCTCTCTCTCTCTCTCTCTCTCG 456
QY 367 CGCCCGCGCGCGCGCGCTTTGGGGGAGAGTCCATCTGTCGCCGAGAGCCGCCGCCCAANTA 426
Db 457 CGCCCGCGCGCGCGCGCTTTGGGGGAGAGTCCATCTGTCGCCGAGAGCCGCCGCCCAANTA 516
QY 427 CAGCATCACTTTACAGGGCAAGTGGAGCCAGACGGGCTTCCCCAAGCAGTACCCCTGTT 486
Db 517 CAGCATCACTTTACAGGGCAAGTGGAGCCAGACGGGCTTCCCCAAGCAGTACCCCTGTT 576
QY 487 CCGCCCCCTGCGCAGTGTCTTTCGCTGTGGGGCGCGGCATAGTCTCCGACTACAGCAT 546
Db 577 CCGCCCCCTGCGCAGTGTCTTTCGCTGTGGGGCGCGGCATAGTCTCCGACTACAGCAT 636
QY 547 GTGGAGGAACCACTAGTACGTACAGTACCGGCTGCGCGACTTTTCCGAGCGCGCGGAGGC 606
Db 637 GTGGAGGAACCACTAGTACGTACAGTACCGGCTGCGCGACTTTTCCGAGCGCGCGGAGGC 696
QY 607 CTGGCGCTGATGAAGAGATCGAGCGCGGGGAGGCGCTGCAGAGCGTGCACGAGGT 666
Db 697 CTGGCGCTGATGAAGAGATCGAGCGCGGGGAGGCGCTGCAGAGCGTGCACGCGGT 756
QY 667 GTTTTTCGGCGCCCGCTCCCGAGCGGACCCGGGAGAGACGTCCGGGAGGTGAGGTGCA 726
Db 757 GTTTTTCGGCGCCCGCTCCCGAGCGGACCCGGGAGAGACGTCCGGGAGGTGAGGTGCA 816
QY 727 GCGCAGGCACTCGCTGCTCTGTTTGTGGTGCATCATGTCGCCAGCCCCGACTGTTCTGT 786
Db 817 GCGCAGGCACTCGCTGCTCTGTTTGTGGTGCATCATGTCGCCAGCCCCGACTGTTCTGT 876
QY 787 GGGCGTGGACAGCTGGACCTGTGCCAGGGGACCGTTGGCGGGAACAGCGCGCTGGA 846
Db 877 GGGCGTGGACAGCTGGACCTGTGCCAGGGGACCGTTGGCGGGAACAGCGCGCTGGA 936
QY 847 CTGTGTACCCCTACGACCGCGGAGCGGACAGCGGCTTACCTTCTCTCTCCCGAACCTTCG 906
Db 937 CCTGTACCCCTACGACCGCGGAGCGGACAGCGGCTTACCTTCTCTCTCCCGAACCTTCG 996
QY 907 CACCATCCCGCAGGACACGGTGACCGAGATAAGCTCTCTCTCCAGCCACCGCGGCAA 966
Db 997 CACCATCCCGCAGGACACGGTGACCGAGATAAGCTCTCTCTCTCCAGCCACCGCGGCAA 1056
QY 967 CTCCTTCTACTACCGCGGCTGAAGGCCCTGCCTCCCATCGCCAGGGGTGACACTGGTGGC 1026

QY 249 GGCTGGACCCGACCGCTGCCGCGCGCTCCCGCTGCTCCTGCGGGTGATGGAAACC 308
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Db 1595 GGGTGGACCCGACCGCTGCCGCGCGCTCCCGCTGCTCCTGCGGGTGATGGAAACC 1536
QY 309 CCAGCCCGCGCGCCCTGGCGAAGGCCCTCTGCGCTCTCCTCTGCGCACTCTCGGG 368
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Db 1535 CCAGCCCGCGCGCCCTGGCGAAGGCCCTCTGCGCTCTCCTCTGCGCACTCTCGGG 1476
QY 369 CCGCGGCCAGCCTCTTGGGGAGAGTCCATCTGTTCCGCCAGAGCCCGCGCAATACA 428
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Db 1475 CCGCGGCCAGCCTCTTGGGGAGAGTCCATCTGTTCCGCCAGAGCCCGCGCAATACA 1416
QY 429 GCATACCTTCACGGGCAAGTGAGCGACAGCGGCCCTTCCCAAGCAGTAGTACCCCTCTTCC 488
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Db 1415 GCATACCTTCACGGGCAAGTGAGCGACAGCGGCCCTTCCCAAGCAGTAGTACCCCTCTTCC 1356
QY 489 GCGCCCTCGCGAGTGGTCTTGCTGCTCTGGGGCGCGCATAGTCCGACTACAGCATGT 548
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Db 1355 GCGCCCTCGCGAGTGGTCTTGCTGCTCTGGGGCGCGCATAGTCCGACTACAGCATGT 1296
QY 549 GGAGGAAGAACCACTACGTACGTAACGGGCTGCGCGACTTTCGGAGCGGGCGGCGCT 608
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Db 1295 GGAGGAAGAACCACTACGTACGTAACGGGCTGCGCGACTTTCGGAGCGGGCGGCGCT 1236
QY 609 GGGCGCTGATGAAGGAGATCGAGCGCGGGGAGGCGCTGCGAGCGTGCACGAGGTGT 668
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Db 1235 GGGCGCTGATGAAGGAGATCGAGCGCGGGGAGGCGCTGCGAGCGTGCACGCGGTGT 1176
QY 669 TTTTGGCGCCCGCCCTCCCGAGCGGACCGGCGAGCGTGGGGAGCTGGAGGTGCAGC 728
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Db 1175 TTTTGGCGCCCGCCCTCCCGAGCGGACCGGCGAGCGTGGGGAGCTGGAGGTGCAGC 1116
QY 729 GCAGGCACTCGCTGCTCGTTTGTGGTGGCATCTGTGCCAGCCCGGCTGTTCTGG 788
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Db 1115 GCAGGCACTCGCTGCTCGTTTGTGGTGGCATCTGTGCCAGCCCGGCTGTTCTGG 1056
QY 789 GCGTGACACGCTTGGACCTGTGGACGGGACCGTTGGCGGGAACAGCGGCGCTGGACC 848
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Db 1055 GCGTGACACGCTTGGACCTGTGGACGGGACCGTTGGCGGGAACAGCGGCGCTGGACC 996
QY 849 TGTACCCCTACGACGCGGGGACGACAGCGGCTTACCTTCTCTCCAGCCACCGGCGCACT 968
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Db 995 TGTACCCCTACGACGCGGGGACGACAGCGGCTTACCTTCTCTCCAGCCACCGGCGCACT 936
QY 909 CCATCCCGCAGGACGCGTGACGAGATACGTCCTCTCTCCAGCCACCGGCGCACT 968
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Db 935 CCATCCCGCAGGACGCGTGACGAGATACGTCCTCTCTCCAGCCACCGGCGCACT 876
QY 969 CTTCTACTACCGCGGCTGAAGGCGCTGCTCCCATCGCAGGCTGACACTGGTGGCG 1028
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Db 875 CTTCTACTACCGCGGCTGAAGGCGCTGCTCCCATCGCAGGCTGACACTGGTGGCG 816
QY 1029 TGGCAGAGACCCCGGCGCTTATCCCTCCCGCCCGAGTCTGCGCAGAGGACAATG 1088
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Db 815 TGGCAGAGACCCCGGCGCTTATCCCTCCCGCCCGAGTCTGCGCAGAGGACAATG 756
QY 1089 AGATTGTAGACAGCGCTCAGTTTCCAGAAAACGCGCTGACACTGCGAGGCTCTCCCTGGT 1148
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Db 755 AGATTGTAGACAGCGCTCAGTTTCCAGAAAACGCGCTGACACTGCGAGGCTCTCCCTGGT 696
QY 1149 CGTCTGGGACTGTGGGAGGCACTGTGGGAGGCTCGGGACCAAGAGCAGGACTCGCT 1208
|||||
Db 695 CGTCTGGGACTGTGGGAGGCACTGTGGGAGGCTCGGGACCAAGAGCAGGACTCGCT 636
QY 1209 ACCTCCGGGTCCAGCCCGCCCAACAGCGGAGCCCTGCCCGAGCTCGAAGAGAGGCTG 1268
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Db 635 ACCTCCGGGTCCAGCCCGCCCAACAGCGGAGCCCTGCCCGAGCTCGAAGAGAGGCTG 576
QY 1269 AGTGCCTCCTGATACTCGGTCTAGACAGAGCCCGGAGCCCTGGGGCCCCCGCGGA 1328
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Db 575 AGTGCCTCCTGATACTCGGTCTAAGACAGAGCCCGGAGCCCTGGGGCCCCCGCGGA 516

QY 1329 GCCATGGGTGTCGGGGGCTCCTGTGCAGGCTCATGCTGCAGGCGCCGAGGCACAGG 1388
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Db 515 GCCATGGGTGTCGGGGGCTCCTGTGCAGGCTCATGCTGCAGGCGCCGAGGCACAGG 456
QY 1389 GGTTCGCGCTGCTCCTGACCGGTTGAGCGCGGCGCCGACCATCTCTGCACTGAAGGGC 1448
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Db 455 GGTTCGCGCTGCTCCTGACCGGTTGAGCGCGGCGCCGACCATCTCTGCACTGAAGGGC 396
QY 1449 CTTCTGGTGGCGCGCAGCGGCATTGGGAAACAGAGCTCCTCTTCCCAACCTTGCTTTA 1508
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Db 395 CTTCTGGTGGCGCGCAGCGGCATTGGGAAACAGAGCTCCTCTTCCCAACCTTGCTTTA 336
QY 1509 GGGGCCCCCGTCTGCTCTCAGGCTCCTCTGAGGATAAAGTCATCCCCA 1568
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Db 335 GGGGCCCCCGTCTGCTCTCAGGCTCCTCTGAGGATAAAGTCATCCCCA 276
QY 1569 AGGCTCCAGCTACTTAAATTAATGCTCTCTTAAATTAATGCTCTGCTCCAGGAGTTGTC 1628
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Db 275 AGGCTCCAGCTACTTAAATTAATGCTCTCTTAAATTAATGCTCTGCTCCAGGAGTTGTC 216
QY 1629 CTTCTATCTCCAGGGGCTGGCTCCACGTTGTCAGATACCTCAGACCTGGTGCTTA 1688
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Db 215 CTTCTATCTCCAGGGGCTGGCTCCACGTTGTCAGATACCTCAGACCTGGTGCTTA 156
QY 1689 GCGTGTGCTGAGCCCACTCTCCGAGGGCGCATCCAAAGCGGGGCCACTTTGAGAGTGAA 1748
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Db 155 GCGTGTGCTGAGCCCACTCTCCGAGGGCGCATCCAAAGCGGGGCCACTTTGAGAGTGAA 96
QY 1749 TAAATGGGCGGTTTCGGAAGCGTCACTGTTTCCATGTTATGAGATCTCTCGGTTTGA 1808
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Db 95 TAAATGGGCGGTTTCGGAAGCGTCACTGTTTCCATGTTATGAGATCTCTCTCGGTTTGA 36
QY 1809 TAAAGACTATCTCTGTTGCTCAAAAAA 1840
|||||
Db 35 TAAAGACTATCTCTGTTGCTCAAAAAA 4
RESULT 4
AAZ34089
ID AAZ34089 standard; cDNA; 1846 BP.
XX
AC AAZ34089;
XX
DT 07-DEC-1999 (first entry)
XX
DE Human PRO866 nucleotide sequence.
DE
KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein; ss.
XX Homo sapiens.
XX
PN WO9946281-A2.
XX
PD 16-SEP-1999.
XX
PF 08-MAR-1999; 99WO-US05028.
XX
PR 10-MAR-1998; 98US-0077450.
PR 11-MAR-1998; 98US-0077632.
PR 11-MAR-1998; 98US-0077641.
PR 11-MAR-1998; 98US-0077649.
PR 12-MAR-1998; 98US-0077791.
PR 13-MAR-1998; 98US-0078004.
PR 17-MAR-1998; 98US-0040220.
PR 20-MAR-1998; 98US-0078886.
PR 20-MAR-1998; 98US-0078910.
PR 20-MAR-1998; 98US-0078936.
PR 20-MAR-1998; 98US-0078939.
PR 25-MAR-1998; 98US-0079294.
PR 26-MAR-1998; 98US-0079656.
PR 27-MAR-1998; 98US-0079663.

PR 27-MAR-1998; 98US-0079664.
PR 27-MAR-1998; 98US-0079689.
PR 27-MAR-1998; 98US-0079728.
PR 27-MAR-1998; 98US-0079786.
PR 30-MAR-1998; 98US-0079920.
PR 30-MAR-1998; 98US-0079923.
PR 31-MAR-1998; 98US-0080105.
PR 31-MAR-1998; 98US-0080107.
PR 31-MAR-1998; 98US-0080165.
PR 31-MAR-1998; 98US-0080194.
PR 01-APR-1998; 98US-0080327.
PR 01-APR-1998; 98US-0080328.
PR 01-APR-1998; 98US-0080333.
PR 01-APR-1998; 98US-0080334.
PR 08-APR-1998; 98US-0081049.
PR 08-APR-1998; 98US-0081070.
PR 09-APR-1998; 98US-0081195.
PR 09-APR-1998; 98US-0081203.
PR 09-APR-1998; 98US-0081229.
PR 15-APR-1998; 98US-0081817.
PR 15-APR-1998; 98US-0081838.
PR 15-APR-1998; 98US-0081952.
PR 15-APR-1998; 98US-0081955.
PR 21-APR-1998; 98US-0082568.
PR 21-APR-1998; 98US-0082569.
PR 22-APR-1998; 98US-0082700.
PR 22-APR-1998; 98US-0082704.
PR 23-APR-1998; 98US-0082804.
PR 23-APR-1998; 98US-0082767.
PR 23-APR-1998; 98US-0082796.
PR 27-APR-1998; 98US-0083336.
PR 28-APR-1998; 98US-0083322.
PR 29-APR-1998; 98US-0083392.
PR 29-APR-1998; 98US-0083495.
PR 29-APR-1998; 98US-0083496.
PR 29-APR-1998; 98US-0083499.
PR 29-APR-1998; 98US-0083500.
PR 29-APR-1998; 98US-0083545.
PR 29-APR-1998; 98US-0083554.
PR 29-APR-1998; 98US-0083558.
PR 29-APR-1998; 98US-0083559.
PR 30-APR-1998; 98US-0083742.
PR 05-MAY-1998; 98US-0084366.
PR 06-MAY-1998; 98US-0084414.
PR 06-MAY-1998; 98US-0084441.
PR 07-MAY-1998; 98US-0084598.
PR 07-MAY-1998; 98US-0084600.
PR 07-MAY-1998; 98US-0084627.
PR 07-MAY-1998; 98US-0084637.
PR 07-MAY-1998; 98US-0084639.
PR 07-MAY-1998; 98US-0084640.
PR 07-MAY-1998; 98US-0084643.
PR 13-MAY-1998; 98US-0085323.
PR 13-MAY-1998; 98US-0085338.
PR 13-MAY-1998; 98US-0085339.
PR 15-MAY-1998; 98US-0085573.
PR 15-MAY-1998; 98US-0085579.
PR 15-MAY-1998; 98US-0085580.
PR 15-MAY-1998; 98US-0085582.
PR 15-MAY-1998; 98US-0085689.
PR 15-MAY-1998; 98US-0085697.
PR 15-MAY-1998; 98US-0085700.
PR 15-MAY-1998; 98US-0085704.
PR 18-MAY-1998; 98US-0086023.
PR 22-MAY-1998; 98US-0086392.
PR 22-MAY-1998; 98US-0086414.
PR 22-MAY-1998; 98US-0086430.
PR 22-MAY-1998; 98US-0086486.
PR 28-MAY-1998; 98US-0087098.
PR 28-MAY-1998; 98US-0087106.
PR 30-JUL-1998; 98US-0094651.
PR

PR 11-SEP-1998; 98US-0100038.
XX
PA (GETH) GENENTECH INC.
XX
PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX
WPI; 1999-551358/46.
DR P-PSDB; AAY41721.
XX

PT New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders -
XX

PS Claim 2; Fig 86; 530pp; English.

XX The present invention describes secreted and transmembrane polypeptides
XX and their polynucleotides. The nucleotide sequences are useful as
CC sources of probes, primers, for chromosome mapping, and for generation
CC of antisense sequences. They can also be used to create transgenic
CC animals. The proteins can be used to treat a variety of diseases and
CC disorders, depending on their function. Diseases that may be treated
CC include blood coagulation disorders, cancers and cellular adhesion
CC disorders. They may also be used to raise antibodies. AA333891 to
CC AA234338, and AAY41685 to AAY41774 represent polynucleotide and
CC polypeptide sequence given in the exemplification of the present
XX invention.

SQ Sequence 1846 BP; 331 A; 622 C; 571 G; 322 T; 0 other;

Query Match 98.5%; Score 1812.8; DB 20; Length 1846;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1814; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 25 GCCAGGGGAAGAGGTGATCCGACCGCGGGAAGGTGCGTGGCAGGCGGAGTTGGGAAG 84
DB 1 GCCAGGGGAAGAGGTGATCCGACCGCGGGAAGGTGCGTGGCAGGCGGAGTTGGGAAG 60
QY 85 CGCGAGCCCCCG 144
DB 61 CGCGAGCCCCCG 120
QY 145 CTCGCTGGAGGCGCAGGCG 204
DB 121 CTCGCTGGAGGCGCAGGCG 180
QY 205 GCCCGGGCG 264
DB 181 GCCCGGGCG 240
QY 265 CTCG 324
DB 241 CTCG 300
QY 325 CTTGGGCAAGGCG 384
DB 301 CTTGGGCAAGGCG 360
QY 385 TGGGGGAGAGTCCATCTGTTCCGCCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 444
DB 361 TGGGGGAGAGTCCATCTGTTCCGCCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
QY 445 CAAAGTGGAGCCAGACGGCG 504
DB 421 CAAAGTGGAGCCAGACGGCG 480
QY 505 GTCTTCGCTGCTGGGGCGTA 564
DB 481 GTCTTCGCTGCTGGGGCGTA 540
QY 565 CGTCAGTAACGGGCTGCG 624
DB 541 CGTCAGTAACGGGCTGCG 600

QY 625 GATCAGAGCGGGGGAGCGCTGCAGAGCGTGCACAGAGTGTCTTTCGGCGCCGCCCT 684
|||||
Db 601 GATCAGAGCGGGGGAGCGCTGCAGAGCGTGCACAGAGTGTCTTTCGGCGCCGCCCT 660
QY 685 CCCAGCGCACCGGCACAGCTCGCGGAGCTGCAGGTGCAGCGCAGCACTCGCTGT 744
|||||
Db 661 CCCAGCGCACCGGCACAGCTCGCGGAGCTGCAGGTGCAGCGCAGCACTCGCTGT 720
QY 745 CTCGTTTGTGTGCGCATCGTCCCGACGCCCGACCTGTTCTGTTGGCGTGGACAGCTGGA 804
|||||
Db 721 CTCGTTTGTGTGCGCATCGTCCCGACGCCCGACCTGTTCTGTTGGCGTGGACAGCTGGA 780
QY 805 CTTGTGCGACGGGAGCGCTTGGCGGGAACAGCGCGCGCTGGACCTGTACCCCTACGACGC 864
|||||
Db 781 CTTGTGCGACGGGAGCGCTTGGCGGGAACAGCGCGCGCTGGACCTGTACCCCTACGACGC 840
QY 865 CGGAGCGACAGCGGTTTACCTTCTCTCCCGCCCACTTCGTCGACCATCCCGCAGGACAC 924
|||||
Db 841 CGGAGCGACAGCGGTTTACCTTCTCTCCCGCCCACTTCGTCGACCATCCCGCAGGACAC 900
QY 925 GGTGACCGAGATAAGCTCTCTCTCCAGCACCGCCGCAACTCTTCTACTACCCGG 984
|||||
Db 901 GGTGACCGAGATAAGCTCTCTCTCCAGCACCGCCGCAACTCTTCTACTACCCGG 960
QY 985 GCTGAAGGCCCTCGCTCCCATCGCAGGCTGACACTGTGTCGGCTCGCAGACAGCCCCAG 1044
|||||
Db 961 GCTGAAGGCCCTCGCTCCCATCGCAGGCTGACACTGTGTCGGCTCGCAGACAGCCCCAG 1020
QY 1045 GGCCTTCATCCTCCCGCCCCAGTCTGCCAGACGAGGACAATGATGTTAGACAGCGC 1104
|||||
Db 1021 GGCCTTCATCCTCCCGCCCCAGTCTGCCAGACGAGGACAATGATGTTAGACAGCGC 1080
QY 1105 CTCAGTTCCAGAAAGCCCTCGACTCGAGCTCTCCCTGTGCTGTGCTGCGGAGCTGTG 1164
|||||
Db 1081 CTCAGTTCCAGAAAGCCCTCGACTCGAGCTCTCCCTGTGCTGTGCTGCGGAGCTGTG 1140
QY 1165 CGGAGGCCACTGTGGAGGCTCGGACCAAGACGAGGACTCGCTACGTCGGGTCCAGCC 1224
|||||
Db 1141 CGGAGGCCACTGTGGAGGCTCGGACCAAGACGAGGACTCGCTACGTCGGGTCCAGCC 1200
QY 1225 CGCACAACAGGAGCCCTCGCCGAGCTCGAAGAAGAGGCTGAGTGGCTCCCTGATAA 1284
|||||
Db 1201 CGCACAACAGGAGCCCTCGCCGAGCTCGAAGAAGAGGCTGAGTGGCTCCCTGATAA 1260
QY 1285 CTGCGTCTAAGACCAAGAGCCCGCAGCCCTCGGCGCCCGCCGAGCCATGGGTGTCGG 1344
|||||
Db 1261 CTGCGTCTAAGACCAAGAGCCCGCAGCCCTCGGCGCCCGCCGAGCCATGGGTGTCGG 1320
QY 1345 GGCTCCTGTGCAGGCTCATGCTGCAGCGCGCGAGGGCACAGGGGTTTTCGGCGTCTGCC 1404
|||||
Db 1321 GGCTCCTGTGCAGGCTCATGCTGCAGCGCGCGAGGGCACAGGGGTTTTCGGCGTCTGCC 1380
QY 1405 TGACCGCGTGAAGCGCGCGCGGACCATCTCTGCACTGAAGGCCCTCTGGTGGCGGCGAC 1464
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Db 1381 TGACCGCGTGAAGCGCGCGCGGACCATCTCTGCACTGAAGGCCCTCTGGTGGCGGCGAC 1440
QY 1465 GGGCATTGGGAACAGCCCTCTCTTCCCAACCTTGCTCTTAGGGCCCCCGTGTCCC 1524
|||||
Db 1441 GGGCATTGGGAACAGCCCTCTCTTCCCAACCTTGCTCTTAGGGCCCCCGTGTCCC 1500
QY 1525 GTCTGCTCTCAGCCCTCTCTCTCGCAGGATAAAGTCATCCCAAGGCTCCAGCTACTCT 1584
|||||
Db 1501 GTCTGCTCTCAGCCCTCTCTCTCGCAGGATAAAGTCATCCCAAGGCTCCAGCTACTCT 1560
QY 1585 AAATTATGTCTCTTATAGTTTATTGCTGCTCCAGGAGATTGCTCTTACGTCTCCAGGG 1644
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Db 1561 AAATTATGTCTCTTATAGTTTATTGCTGCTCCAGGAGATTGCTCTTACGTCTCCAGGG 1620
QY 1645 CTTGGCTCCAGCTGGTTCAGATACCTCAGACCTGGTGCTCTAGGCTGTGTGAGCCCA 1704
|||||
Db 1621 CTTGGCTCCAGCTGGTTCAGATACCTCAGACCTGGTGCTCTAGGCTGTGTGAGCCCA 1680
QY 1705 CTCTCCGAGGGCGCATCCCAAGGGGGCCACTTGAGAAGTGAATAAATGGGCGGTTTC 1764

Db 1681 CTCTCCCGAGGCGCATCCAAAGCGGGCCACTTGAGAAGTGAATAAATGGGCGGTTTC 1740
QY 1765 GGAAGCGTCAGTGTTCATGTTATGGATCTCTCTGCGTTTGAATAAAGACTATCTCTGT 1824
|||||
Db 1741 GGAAGCGTCAGTGTTCATGTTATGGATCTCTCTGCGTTTGAATAAAGACTATCTCTGT 1800
QY 1825 TGCTCAAAAAA 1840
|||||
Db 1801 TGCTCAAAAAA 1816
RESULT 5
AAC78507
ID AAC78507 standard; cDNA; 1847 BP.
XX
AC AAC78507;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human PRO866 (UNQ435) nucleotide sequence SEQ ID NO:235.
XX
KW Human; secreted protein; transmembrane protein; PRO; EST; cytosstatic;
XX expressed sequence tag; detection; cancer; ss.
OS Homo sapiens.
XX
PN WO200053756-A2.
XX
PD 14-SEP-2000.
XX
PF 18-FEB-2000; 2000WO-US04341.
XX
PR 08-MAR-1999; 99WO-US05028.
PR 12-MAR-1999; 99US-0123957.
PR 29-MAR-1999; 99US-0126773.
PR 21-APR-1999; 99US-0130232.
PR 28-APR-1999; 99US-0131445.
PR 14-MAY-1999; 99US-0134287.
PR 23-JUN-1999; 99US-0141037.
PR 26-JUL-1999; 99US-0145698.
PR 29-OCT-1999; 99US-0162506.
PR 30-NOV-1999; 99WO-US28313.
PR 02-DEC-1999; 99WO-US28511.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
XX
PA (GEPH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Kijavoin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2000-611443/58.
DR P-PSDB; AAB44277.
XX
PT Novel PRO polypeptides and polynucleotides used in detection methods,
PT to target bioactive molecules to specific cells, and to modulate
PT cellular activities .
XX
PS Claim 2; Fig 86; 636pp; English.
XX
CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed
CC sequence tag) sequences which encode secreted or transmembrane PRO
CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic
CC activity. The polynucleotides and polypeptides can be used for detecting

CC the presence of PRO polypeptides in samples, for linking bioactive
CC molecules to cells and for modulating biological activities of cells,
CC using the polypeptides for specific targeting. The polypeptide targeting
CC can be used to kill the target cells, e.g. for the treatment of cancers.
CC The polypeptide pairs provide specific targeting of bioactive molecules
CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
CC the isolation of the PRO polynucleotide sequences.
XX
SQ Sequence 1847 BP; 332 A; 622 C; 571 G; 322 T; 0 other;

Query Match		98.5%;	Score 1812.8;	DB 21;	Length 1847;
Best Local Similarity		99.9%;	Pred. No. 0;		
Matches 1814;		Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	25	GCCAGGGGAAGAGGGTATCCGACCCGGGGAAGGTCCGTGGGCAGGCGGAGTTGGGAAG	84		
DB	1	GCCAGGGGAAGAGGGTATCCGACCCGGGGAAGGTCCGTGGGCAGGCGGAGTTGGGAAG	60		
QY	85	CGGAGCCCCCGCGCGCCCGGAGCCCTTCTCCTCTTCTCCACGTCCTATCTGCCT	144		
DB	61	CGGAGCCCCCGCGCGCCCGGAGCCCTTCTCCTCTTCTCCACGTCCTATCTGCCT	120		
QY	145	CTCGCTGGAGGCCAGCGCTGCAGCATCGAAGACAGAGGAACTGAGCCTCATTTGGCGG	204		
DB	121	CTCGCTGGAGGCCAGCGCTGCAGCATCGAAGACAGAGGAACTGAGCCTCATTTGGCGG	180		
QY	205	GCCCGGGGGCCGGCCTCGGGCTTAAATAGGAGCTCCGGCTCTGGCTGGGACCCGACCG	264		
DB	181	GCCCGGGGGCCGGCCTCGGGCTTAAATAGGAGCTCCGGCTCTGGCTGGGACCCGACCG	240		
QY	265	CTGCGGGCGCGCTCCCGCTGCTCTGCGGGTGATGGAACCCAGCCCGCGCCCGC	324		
DB	241	CTGCGGGCGCGCTCCCGCTGCTCTGCGGGTGATGGAACCCAGCCCGCGCCCGC	300		
QY	325	CTTGGCAAGGGCCCTTGGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	384		
DB	301	CTTGGCAAGGGCCCTTGGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	360		
QY	385	TGGGGGAGAGTCCATCTGTTCGCCAGAGCCCGGCAAAATACAGCATCACCTTCACGGG	444		
DB	361	TGGGGGAGAGTCCATCTGTTCGCCAGAGCCCGGCAAAATACAGCATCACCTTCACGGG	420		
QY	445	CAAGTGGAGCCAGAGCGCTTCCCAAGCAGTACCCCTCTGTCGCCGCCCTCGCGCAGTG	504		
DB	421	CAAGTGGAGCCAGAGCGCTTCCCAAGCAGTACCCCTCTGTCGCCGCCCTCGCGCAGTG	480		
QY	505	GTCTTCGCTGCTGGGGCGCGCATAGCTCCGACTACAGCATGTGAGGAAGAACAGTA	564		
DB	481	GTCTTCGCTGCTGGGGCGCGCATAGCTCCGACTACAGCATGTGAGGAAGAACAGTA	540		
QY	565	CGTCAGTAACGGGCTCGGGACTTTTCGGAGCGCGGAGGCTGGGCGCTGATGAAGGA	624		
DB	541	CGTCAGTAACGGGCTCGGGACTTTTCGGAGCGCGGAGGCTGGGCGCTGATGAAGGA	600		
QY	625	GATCGAGCGGGGGAGGCGCTGCAGAGCGTGACAGAGGTGTTTTCGGCGCCCGCCCT	684		
DB	601	GATCGAGCGGGGGAGGCGCTGCAGAGCGTGACAGAGGTGTTTTCGGCGCCCGCCCT	560		
QY	685	CCGACGCGCACCGGCGAGACGCTCGGCGAGCTGGAGGTGCAGCGCAGCATCTCGTGT	744		
DB	661	CCGACGCGCACCGGCGAGACGCTCGGCGAGCTGGAGGTGCAGCGCAGCATCTCGTGT	720		
QY	745	CTCGTTTGTGTCGCATCGTGCCAGCCCGGACTGGTTCTGTTGGGCGTGACAGCCTGGA	804		
DB	721	CTCGTTTGTGTCGCATCGTGCCAGCCCGGACTGGTTCTGTTGGGCGTGACAGCCTGGA	780		
QY	805	CCTGTCGAGGGGACCGTTGGGGGAAACAGGCGGCGCTGGAGCCTGTACCCCTACGACGC	864		
DB	781	CCTGTCGAGGGGACCGTTGGGGGAAACAGGCGGCGCTGGAGCCTGTACCCCTACGACGC	840		
QY	865	CGGAGCGGACAGCGGCTTCACTTCTCTCCCGCAACTTCGCCACCATCCCGCAGGACAC	924		
DB	841	CGGAGCGGACAGCGGCTTCACTTCTCTCCCGCAACTTCGCCACCATCCCGCAGGACAC	900		

QY	925	GGTGACCGGAGATAACGTCTCTCTCTCCAGCCACCGGCAACTCTTCTACTACCGCG	984
DB	901	GGTGACCGGAGATAACGTCTCTCTCTCCAGCCACCGGCAACTCTTCTACTACCGCG	960
QY	985	GCTGAAGGCCCTGCTCCATCGCAGGTGACACTGTGTGGCTGCGACAGAGCCCCAG	1044
DB	961	GCTGAAGGCCCTGCTCCATCGCAGGTGACACTGTGTGGCTGCGACAGAGCCCCAG	1020
QY	1045	GGCTTTCATCCCTCCCGCCCCAGTCTGCCAGCAGGACAATGAGATTGTAGACAGCG	1104
DB	1021	GGCTTTCATCCCTCCCGCCCCAGTCTGCCAGCAGGACAATGAGATTGTAGACAGCG	1080
QY	1105	CTCAGTTCCAGAAACCGCTGGACTGCGAGGTCTCCCTGTGTCTCTCTGGGACTGTG	1164
DB	1081	CTCAGTTCCAGAAACCGCTGGACTGCGAGGTCTCCCTGTGTCTCTCTGGGACTGTG	1140
QY	1165	CGGAGGCCACTGTGGGAGCTCTGGGACCAAGAGCAGACTCGCTACGTCGGGTCCAGCC	1224
DB	1141	CGGAGGCCACTGTGGGAGCTCTGGGACCAAGAGCAGACTCGCTACGTCGGGTCCAGCC	1200
QY	1225	CGCCAAACGGGAGGCCCTGCCCCAGCTCGAAGAAGAGGCTGAGTGGTCCCTGATAA	1284
DB	1201	CGCCAAACGGGAGGCCCTGCCCCAGCTCGAAGAAGAGGCTGAGTGGTCCCTGATAA	1260
QY	1285	CTGCGTCTAAGACACAGAGCCCGCGAGCCCTGGGGCCCCCGGAGCCATGGGTGTGCGG	1344
DB	1261	CTGCGTCTAAGACACAGAGCCCGCGAGCCCTGGGGCCCCCGGAGCCATGGGTGTGCGG	1320
QY	1345	GGTCTCTGTGAGGCTCATGTGTCAGGCGGCGAGGGACAGAGGGGTTCGGGCTGCTCC	1404
DB	1321	GGTCTCTGTGAGGCTCATGTGTCAGGCGGCGAGGGACAGAGGGGTTCGGGCTGCTCC	1380
QY	1405	TGACCGCGGTGAGGCGCGCGACCATCTCTGCACGTGAAGGCGCCCTCTGCTGGCGGAC	1464
DB	1381	TGACCGCGGTGAGGCGCGCGACCATCTCTGCACGTGAAGGCGCCCTCTGCTGGCGGAC	1440
QY	1465	GGGCATTGGGAACACAGCCCTCTCTTCCCAACCTTTCCTTAGGGGCCCCCGGTGCC	1524
DB	1441	GGGCATTGGGAACACAGCCCTCTCTTCCCAACCTTTCCTTAGGGGCCCCCGGTGCC	1500
QY	1525	GTCTGCTCTCAGCCTCCTCTCTGTCAGGATAAAGTCATCCCCAAGGCTCCAGCTACTCT	1584
DB	1501	GTCTGCTCTCAGCCTCCTCTCTGTCAGGATAAAGTCATCCCCAAGGCTCCAGCTACTCT	1560
QY	1585	AAATTATGTCCTTATTAAGTTATTGCTCTCCAGGAGATTGCTTCATCGTCCAGGG	1644
DB	1561	AAATTATGTCCTTATTAAGTTATTGCTCTCCAGGAGATTGCTTCATCGTCCAGGG	1620
QY	1645	CCTGGCTCCAGCTGGTTGCAGATACCTCAGACCTGGTCTCTAGGCTGTGCTAGGCCA	1704
DB	1621	CCTGGCTCCAGCTGGTTGCAGATACCTCAGACCTGGTCTCTAGGCTGTGCTAGGCCA	1680
QY	1705	CTCTCCGAGGCGCATCCAAAGCGGGGCGACTTGAGAAGTGAATAAATGGGGCGGTTTC	1764
DB	1681	CTCTCCGAGGCGCATCCAAAGCGGGGCGACTTGAGAAGTGAATAAATGGGGCGGTTTC	1740
QY	1765	GGAAGGTCAGTGTTCCTATTAAGTTATTGATGATCTCTGCGTTTGAATAAAGACTATCTCTG	1824
DB	1741	GGAAGGTCAGTGTTCCTATTAAGTTATTGATGATCTCTGCGTTTGAATAAAGACTATCTCTG	1800
QY	1825	TGCTCAAAAAAANA 1840	
DB	1801	TGCTCAAAAAAANA 1816	

RESULT 6
AAC58630
ID AAC58630 standard; cDNA; 1847 BP.
XX
AC AAC58630;
XX
DT 29-JAN-2001 (first entry)


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QY 625 GATCGAGCGCGGGAGCGCTGCAGAGCGTGCACGAGGTGTTTTCGGCGCCCGCCGT 684
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Db 601 GATCGAGCGCGGGAGCGCTGCAGAGCGTGCACGAGGTGTTTTCGGCGCCCGCCGT 660
QY 685 CCGCAGCGCAGCGGCGCAGCGTGCAGAGCGTGCAGAGGTGTTTTCGGCGCCCGCCGT 744
|||||
Db 661 CCGCAGCGCAGCGGCGCAGCGTGCAGAGCGTGCAGAGGTGTTTTCGGCGCCCGCCGT 720
QY 745 CTCGTTTGTGTCGATCGTCCCGAGCGCCGACGTCGTTGTCGTCGCGTGCAGCGTGA 804
|||||
Db 721 CTCGTTTGTGTCGATCGTCCCGAGCGCCGACGTCGTTGTCGTCGCGTGCAGCGTGA 780
QY 805 CTTGTGCGACGGGACCGTGTGGCGGGAACAGCGCGCGCTGGACCTGTACCCCTACGACGC 864
|||||
Db 781 CTTGTGCGACGGGACCGTGTGGCGGGAACAGCGCGCGCTGGACCTGTACCCCTACGACGC 840
QY 865 CGGAGCGACAGCGGTTTCCCTTCTCTCCCGGAGTGTGTCGCGCTCGACAGAGCCCGAG 924
|||||
Db 841 CGGAGCGACAGCGGTTTCCCTTCTCTCCCGGAGTGTGTCGCGCTCGACAGAGCCCGAG 900
QY 925 GTGACCGAGATAAGTCTCTCTCCCGAGCGCCGACGTCGTTGTCGTCGCGTGCAGCGTGA 984
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Db 901 GTGACCGAGATAAGTCTCTCTCCCGAGCGCCGACGTCGTTGTCGTCGCGTGCAGCGTGA 960
QY 985 GCTGAAGGCCCTGCTCCCATCCGAGGCTGACACTGTGTCGCGCTCGACAGAGCCCGAG 1044
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Db 961 GCTGAAGGCCCTGCTCCCATCCGAGGCTGACACTGTGTCGCGCTCGACAGAGCCCGAG 1020
QY 1045 GGCCTTATCTCTCCCGCCCGAGTCTCTCCCGAGCGGACAAATGATGTTAGACAGCGC 1104
|||||
Db 1021 GGCCTTATCTCTCCCGCCCGAGTCTCTCCCGAGCGGACAAATGATGTTAGACAGCGC 1080
QY 1105 CTCAGTTCAGAAACCGCTGACTGCGAGCTCTCCCTGTGTCGTCGTCGGGACTGTG 1164
|||||
Db 1081 CTCAGTTCAGAAACCGCTGACTGCGAGCTCTCCCTGTGTCGTCGTCGGGACTGTG 1140
QY 1165 CGGAGGCCACTGTGGAGGCTCGGACCAAGACGAGCTCTGCTCGCGGTCCAGCC 1224
|||||
Db 1141 CGGAGGCCACTGTGGAGGCTCGGACCAAGACGAGCTCTGCTCGCGGTCCAGCC 1200
QY 1225 CGCACAACAGGAGCCCTGCGCCGAGCTCGAAGAAGGTGAGTGCCTCCCTGATAA 1284
|||||
Db 1201 CGCACAACAGGAGCCCTGCGCCGAGCTCGAAGAAGGTGAGTGCCTCCCTGATAA 1260
QY 1285 CTGCGTCTAAGACAGAGCCCGAGCCCTGCGGCCCGCCGAGCATGGGTGTCGGG 1344
|||||
Db 1261 CTGCGTCTAAGACAGAGCCCGAGCCCTGCGGCCCGCCGAGCATGGGTGTCGGG 1320
QY 1345 GGCTCCTGTGCAAGGCTCATGCTGCAGGGCGCGAGGGCACAGGGGTTTTCGCGCTGCTCC 1404
|||||
Db 1321 GGCTCCTGTGCAAGGCTCATGCTGCAGGGCGCGAGGGCACAGGGGTTTTCGCGCTGCTCC 1380
QY 1405 TCAGCGCGTGAAGCGCGCGCGACCATCTCTGCAGTGAAGGCGCCCTCTGGTGGCGCGCAC 1464
|||||
Db 1381 TCAGCGCGTGAAGCGCGCGCGACCATCTCTGCAGTGAAGGCGCCCTCTGGTGGCGCGCAC 1440
QY 1465 GGGCATTTGGAAACAGCCTCTCTCTCCCAACCTTGTCTTAGGGGCCCGCGTCTCC 1524
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Db 1441 GGGCATTTGGAAACAGCCTCTCTCTCCCAACCTTGTCTTAGGGGCCCGCGTCTCC 1500
QY 1525 GTCTGCTCTCAGCCTCTCTCTCTCAGGATTAAGTCAATPCCCAAGGCTTCCAGCTACTCT 1584
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Db 1501 GTCTGCTCTCAGCCTCTCTCTCTCAGGATTAAGTCAATPCCCAAGGCTTCCAGCTACTCT 1560
QY 1585 AAATTATGCTCTTATAGTTATTGCTGCTCCAGAGATTGCTCTCATCTCCAGGGG 1644
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Db 1561 AAATTATGCTCTTATAGTTATTGCTGCTCCAGAGATTGCTCTCATCTCCAGGGG 1620
QY 1645 CTGGCTCCCGAGTGTGTCAGATACCTCAGACCTGGTCTCTAGGCTGTGCTGAGCCCA 1704
|||||
Db 1621 CTGGCTCCCGAGTGTGTCAGATACCTCAGACCTGGTCTCTAGGCTGTGCTGAGCCCA 1680
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QY 1705 CTCTCCCGAGGCGCATCCAAAGCGGGGCCACTTGCAGAGTGAATAAATGGGCGGTTTC 1764
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Db 1681 CTCTCCCGAGGCGCATCCAAAGCGGGGCCACTTGCAGAGTGAATAAATGGGCGGTTTC 1740
QY 1765 GGAAGCGTCAGTGTTCATGTTATGGATCTCTCTGCGTTTGAATAAAGACTATCTCTGT 1824
|||||
Db 1741 GGAAGCGTCAGTGTTCATGTTATGGATCTCTCTGCGTTTGAATAAAGACTATCTCTGT 1800
QY 1825 TGCTCAAAAAA 1840
|||||
Db 1801 TGCTCAAAAAA 1816

RESULT 7
AAA49728
ID AAA49728 standard; cDNA; 1847 BP.
XX AC AAA49728;
XX XX
XX DT 25-SEP-2000 (first entry)
XX DE Human PRO866 cDNA clone DNA53971-1359.
XX KW PRO866; human; antitumour; tumour; therapy; cytostatic;
KW breast cancer; ovarian cancer; renal cancer; colorectal cancer;
KW uterine cancer; prostate cancer; lung cancer; bladder cancer;
KW central nervous system cancer; melanoma; leukaemia; neoplasia; ss.
XX OS Homo sapiens.
XX Key Location/Qualifiers
FH CDS 275..1270
FT sig_peptide /*tag= a
FT /*tag= b
FT mat_peptide 275..352
FT /*tag= c
XX WO200037638-A2.
XX PD 29-JUN-2000.
XX PF 02-DEC-1999; 99WO-US28565.
XX PR 22-DEC-1998; 98US-0113296.
XX PR 08-MAR-1999; 99WO-US05028.
XX PR 21-APR-1999; 99US-0130232.
XX PR 28-APR-1999; 99US-0131445.
XX PR 14-MAY-1999; 99US-0134287.
XX PR 20-JUL-1999; 99US-0144758.
XX PR 26-JUL-1999; 99US-0145698.
XX PR 15-SEP-1999; 99WO-US21090.
XX PR 15-SEP-1999; 99WO-US21547.
XX (GETH ) GENENTECH INC.
XX PI Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Marsters SA;
PI Napier MA, Pitti RM, Wood WI;
XX WPI: 2000-442668/38.
DR P-PSDB; AAY95349.
XX Novel composition to inhibit neoplastic cell growth or for treating
XX tumor in mammal comprises polypeptides PRO179, PRO207, PRO320, PRO219,
XX PRO221, PRO224, PRO328, PRO301, PRO526, PRO362, PRO356, PRO309 or
XX PRO866.
XX PS Claim 20; Fig 25; 172pp; English.
XX The present sequence is that of cDNA clone DNA53971-1359
CC (ATCC 209750) encoding human PRO866 (see AAY95349), a novel antitumour
CC protein showing similarity to mindin/spondin proteins. The cDNA
CC was isolated from a human foetal kidney cDNA library by hybridisation.
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CC A claimed method for inhibiting the growth of a tumour cell comprises
CC exposing the tumor cell to PRO179, PRO207, PRO320, PRO321, PRO221,
CC PRO224, PRO328, PRO301, PRO356, PRO356, PRO509 or PRO866 (see
CC AAY95337-49), their agonists or chimeric polypeptides incorporating
CC them. The tumour is especially a cancer selected from breast,
CC ovarian, renal, colorectal, uterine, prostate, lung, bladder and
CC central nervous system cancer, melanoma and leukaemia. Nucleic
CC acids encoding PRO179 etc. are used in the recombinant production
CC of the antitumour polypeptides.
XX
SQ Sequence 1847 BP; 332 A; 622 C; 571 G; 322 T; 0 other;

Query Match 98.5%; Score 1812.8; DB 21; Length 1847;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1814; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	25	GCACGGGAAGAGGGTGATCCGACCCGGGAAGGTGCTGGGGAGGGGAGTTGGGAAG	84
DB	1	GCACGGGAAGAGGGTGATCCGACCCGGGAAGGTGCTGGGGAGGGGAGTTGGGAAG	60
QY	85	CGGACGCCCGCGCCCGCGGAGCCCTTCTCCTCTTCTCCACGTCCTATCTGCCT	144
DB	61	CGGACGCCCGCGCCCGCGGAGCCCTTCTCCTCTTCTCCACGTCCTATCTGCCT	120
QY	145	CTCGCTGGAGCCAGGCGCTGACATCGAAGACAGGAGGAAGTGAATGGCCG	204
DB	121	CTCGCTGGAGCCAGGCGCTGACATCGAAGACAGGAGGAAGTGAATGGCCG	180
QY	205	GGCCGGGGCGCGCTCGGCGCTTAATAGGAGCTCGGGCTTGGTGGAACCCGACG	264
DB	181	GGCCGGGGCGCGCTCGGCGCTTAATAGGAGCTCGGGCTTGGTGGAACCCGACG	240
QY	265	CTCGGCGCGCTCGGCGCTTCTCGCGGCTGATGGAAGAACCCGACGCGCCGCG	324
DB	241	CTCGGCGCGCTCGGCGCTTCTCGCGGCTGATGGAAGAACCCGACGCGCCGCG	300
QY	325	CTTGGGCAAGCGCTCTGCGCTCTCTCTGCGCACTCTCGGCGCGCGCGCGCGCT	384
DB	301	CTTGGGCAAGCGCTCTGCGCTCTCTCTGCGCACTCTCGGCGCGCGCGCGCT	360
QY	385	TGGGGAGAGTCCATCTGTTTCCGCGAGAGCCCGCGGCAATACAGATACCTTCAGGG	444
DB	361	TGGGGAGAGTCCATCTGTTTCCGCGAGAGCCCGCGGCAATACAGATACCTTCAGGG	420
QY	445	CAAGTGAGCCAGAGGCGCTTCCCAAGCAGTACCCCTCTTCCGCGCGCGCGCGAGTG	504
DB	421	CAAGTGAGCCAGAGGCGCTTCCCAAGCAGTACCCCTCTTCCGCGCGCGCGAGTG	480
QY	505	GTCTTCGCTGCTGGGGCGCGCATAGCTCCGACTACAGCATGTGGAGGAAGAACAGTA	564
DB	481	GTCTTCGCTGCTGGGGCGCGCATAGCTCCGACTACAGCATGTGGAGGAAGAACAGTA	540
QY	565	CGTCAGTAAGGGCTGCGGACCTTTCGGAGCGCGGGAGGCGCTGGGCGCTGATGAAGGA	624
DB	541	CGTCAGTAAGGGCTGCGGACCTTTCGGAGCGCGGGAGGCGCTGGGCGCTGATGAAGGA	600
QY	625	GATCGAGGCGCGGGAGGCGCTGCGAGAGCTGCGAGAGGCTTTCGCGCGCGCGCGT	684
DB	601	GATCGAGGCGCGGGAGGCGCTGCGAGAGCTGCGAGAGGCTTTCGCGCGCGCGCGT	660
QY	685	CCCCAGCGGCGGCGGAGAGCTCGGCGAGCTGGAGGTGCGAGCGAGGCACTCGTGGT	744
DB	661	CCCCAGCGGCGGCGGAGAGCTCGGCGAGCTGGAGGTGCGAGCGAGGCACTCGTGGT	720
QY	745	CTCGTTTGTGGTGGGATCTGCGGCGGAGCGGCGGAGCTGGTTCGTTGGGCGTGAACCTGGA	804
DB	721	CTCGTTTGTGGTGGGATCTGCGGCGGAGCGGCGGAGCTGGTTCGTTGGGCGTGAACCTGGA	780
QY	805	CTCTCGGAGCGGCGGTTGGGGAAGAGCGGCGGCTGAGCTGTACCCCTACGACGC	864
DB	781	CTCTCGGAGCGGCGGTTGGGGAAGAGCGGCGGCTGAGCTGTACCCCTACGACGC	840
QY	865	CGGAGCGGAGCGGCTTACCTTCTCTCCGCCAACTTCCGCCACCATCCCGAGGACAC	924

DB	841	CGGGAGCGGACAGCGGCTTACCTTCTCCTCCCAACTTCGCCACCATCCCGGAGGACAC	900
QY	925	GGTGACCGAGATTAACCTCTCTCTCCAGCACCGCGCAACTCTTCTACTACCGCG	984
DB	901	GGTGACCGAGATTAACCTCTCTCTCCAGCACCGCGCAACTCTTCTACTACCGCG	960
QY	985	GCTGAAGGCGCTGCTTCCATCGCCAGGGTGACACTGGTGCGGCTCGACAGAGCCCCAG	1044
DB	961	GCTGAAGGCGCTGCTTCCATCGCCAGGGTGACACTGGTGCGGCTCGACAGAGCCCCAG	1020
QY	1045	GGCTTTATCTCTCCCGCCCCAGTCTCTGCCAGCGGACAAATGAGATTGTAGACAGCG	1104
DB	1021	GGCTTTATCTCTCCCGCCCCAGTCTCTGCCAGCGGACAAATGAGATTGTAGACAGCG	1080
QY	1105	CTCAGTTCCAGAAACCGCGCTGACTGGAGGTCTCCCTGTGTCTCTGGGAGCTGTG	1164
DB	1081	CTCAGTTCCAGAAACCGCGCTGACTGGAGGTCTCCCTGTGTCTCTGGGAGCTGTG	1140
QY	1165	CGGAGGCCACTGTGGAGGCTCGGGACCAAGAGCAGGACTCGCTACGTCCGGGTCCAGCC	1224
DB	1141	CGGAGGCCACTGTGGAGGCTCGGGACCAAGAGCAGGACTCGCTACGTCCGGGTCCAGCC	1200
QY	1225	CGCCAAACAGGGAGGCCCTCGCCCGAGCTCGAAGAGAGGCTGAGTGGCTCCCTGATAA	1284
DB	1201	CGCCAAACAGGGAGGCCCTCGCCCGAGCTCGAAGAGAGGCTGAGTGGCTCCCTGATAA	1260
QY	1285	CTCGCTTAAGACCAGAGCCCGCGAGCCCTGGGGCCCCCGGAGGACATGGGCTGCGG	1344
DB	1261	CTCGCTTAAGACCAGAGCCCGCGAGCCCTGGGGCCCCCGGAGGACATGGGCTGCGG	1320
QY	1345	GGCTCTGTGAGGCTCATGTCTGAGCGCGCGGAGGACAGGGGTTTCGCGCTGCTCC	1404
DB	1321	GGCTCTGTGAGGCTCATGTCTGAGCGCGCGGAGGACAGGGGTTTCGCGCTGCTCC	1380
QY	1405	TGACCGCGGTGAGGCGCGCGGACCATCTCTGCACCTGAAGGGCCCTCTGTTGGTCCGCGCAC	1464
DB	1381	TGACCGCGGTGAGGCGCGCGGACCATCTCTGCACCTGAAGGGCCCTCTGTTGGTCCGCGCAC	1440
QY	1465	GGCATTTGGGAACAGGCTCTCTTCCCAACTTGTCTTTCAGGGCCCCCGTGTCC	1524
DB	1441	GGCATTTGGGAACAGGCTCTCTTCCCAACTTGTCTTTCAGGGCCCCCGTGTCC	1500
QY	1525	GTCTGTCTCAGGCTCTCTCTCTGAGGATAAAGTCAATCCCAAGGCTCCAGTACTCT	1584
DB	1501	GTCTGTCTCAGGCTCTCTCTCTGAGGATAAAGTCAATCCCAAGGCTCCAGTACTCT	1560
QY	1585	AAATTATGTCTCTTATAAGTTATTGCTGCTCCAGGAGATTGCTTCATGTCAGGGG	1644
DB	1561	AAATTATGTCTCTTATAAGTTATTGCTGCTCCAGGAGATTGCTTCATGTCAGGGG	1620
QY	1645	CTTGGCTCCACGCTGTTGAGATACCTCAGACCTGGTGTCTAGGCTGTGCTGAGGCCA	1704
DB	1621	CTTGGCTCCACGCTGTTGAGATACCTCAGACCTGGTGTCTAGGCTGTGCTGAGGCCA	1680
QY	1705	CTCTCCCGGGGCGCATCCAAAGCGGGGCGACCTTGAGAAGTGAATAAATGGGCGGTTTC	1764
DB	1681	CTCTCCCGGGGCGCATCCAAAGCGGGGCGACCTTGAGAAGTGAATAAATGGGCGGTTTC	1740
QY	1765	GGAAGGCTCAGTGTTCCTCATCTCTGCTTATGATCTCTCTGCTTTGAATAAAGACTATCTGT	1824
DB	1741	GGAAGGCTCAGTGTTCCTCATCTCTGCTTATGATCTCTCTGCTTTGAATAAAGACTATCTGT	1800
QY	1825	TGCTCAAAAAAAAAA 1840	
DB	1801	TGCTCAAAAAAAAAA 1816	

RESULT 8
AAK94244
ID AAK94244 standard; cDNA; 1798 BP.
XX
AC AAK94244;

XX 06-NOV-2001 (first entry)
XX Human full-length cDNA, SEQ ID NO: 2846.
XX Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
XX Homo sapiens.
OS EP1130094-A2.
XX 05-SEP-2001.
XX 07-JUL-2000; 2000EP-0114089.
XX 08-JUL-1999; 99JP-0194486.
PR 11-JAN-2000; 2000JP-0118774.
PR 02-MAY-2000; 2000JP-01183765.
XX (HELI-) HELIX RES INST.
XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX WPI; 2001-524355/58.
DR P-PSDB; AAM93324.
XX 830 Primers useful for synthesizing full length cDNA clones and their
PT use in genetic manipulation -
XX Claim 8; SEQ ID NO 2846; 1380pp + sequence listing; English.
XX The invention relates to primers for synthesising full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been
CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
CC molecules have been determined. Primers for synthesising the full length
CC cDNA are useful for clarifying the function of the protein encoded by
CC the cDNA. The full length clones were obtained by construction of full
CC length enriched cDNA libraries that were synthesised by the oligo-capping
CC method. The primers enable the production of the full length cDNA easily
CC without any special methods. The present sequence is a full length
CC human cDNA of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in CD-ROM format directly from EPO.
XX Sequence 1798 BP; 291 A; 619 C; 566 G; 322 T; 0 other;
SQ
Query Match 97.5%; Score 1793.2; DB 22; Length 1798;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1795; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 32 GAAGAGGGTGATCCGACCCGGGAGGTGCGTGGGAGGGGAGTTGGGAAAGCGGCAGC 91
DB 1 GAAGAGGGTGATCCGACCCGGGAGGTGCGTGGGAGGGGAGTTGGGAAAGCGGCAGC 60
QY 92 CCCCGCGCCCGCGAGCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 151
DB 61 CCCCGCGCCCGCGAGCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 152 GAGGCGAGGCGGTGAGCATCGAAGACAGAGAACTGAGGCTCATTTGGCGGCCCGGG 211
DB 121 GAGGCGAGGCGGTGAGCATCGAAGACAGAGAACTGAGGCTCATTTGGCGGCCCGGG 180
QY 212 GCGCGGCGCTCGGGCTTAATAGGAGCTCCGGCTCTGGCTGGAGCCCGACCGCTCCCGG 271
DB 181 GCGCGGCGCTCGGGCTTAATAGGAGCTCCGGCTCTGGCTGGAGCCCGACCGCTCCCGG 240
QY 272 CCGCGCTCCCGCTGCT 331
DB 241 CCGCGCTCCCGCTGCT 300
QY 332 AAGGCCCTCTGGCT 391
DB 1798 BP; 291 A; 619 C; 566 G; 322 T; 0 other;

DB 301 AAGGCCCTCTGGCT 360
QY 392 GAGTCCATCTGTTCCGCGAGAGCCCGGCAAAATACAGCATCACCTTACGGGCAAGTGG 451
DB 361 GAATCCATCTGTTCCGCGAGAGCCCGGCAAAATACAGCATCACCTTACGGGCAAGTGG 420
QY 452 AGCCAGAGCGGCTTCCCAAGCAGTACCCCTGTTTCCGCGCCCTTCCGCGAGTGGTCTTCG 511
DB 421 AGCCAGAGCGGCTTCCCAAGCAGTACCCCTGTTTCCGCGCCCTTCCGCGAGTGGTCTTCG 480
QY 512 CTGCTGGGGGCGCGCATAGCTCCGCTACAGCATGATGAGGAGAAACAGTACGTCAGT 571
DB 481 CTGCTGGGGGCGCGCATAGCTCCGCTACAGCATGATGAGGAGAAACAGTACGTCAGT 540
QY 572 AACGGGCTCGCGACTTTCGGAGCGCGGAGGCTTGGGCGCTGATGAAGAGATCGAG 631
DB 541 AACGGGCTCGCGACTTTCGGAGCGCGGAGGCTTGGGCGCTGATGAAGAGATCGAG 600
QY 632 GCGGGGCGGAGGCGCTGCGAGAGCGTGCACGAGGTGTTTTCGGGCGCCCTTCCCAAGC 691
DB 601 GCGGGGCGGAGGCGCTGCGAGAGCGTGCACGAGGTGTTTTCGGGCGCCCTTCCCAAGC 660
QY 692 GGCACCGGCGACAGTCCGCGGAGCTGAGGCTGACGCGAGGACTCGCTGGTCTCGTTT 751
DB 661 GGCACCGGCGACAGTCCGCGGAGCTGAGGCTGACGCGAGGACTCGCTGGTCTCGTTT 720
QY 752 GTGGTGCATCTGTCGCCAGCCGACTGTTGCTGGGCTGGACAGCTGACAGCTGTGC 811
DB 721 GTGGTGCATCTGTCGCCAGCCGACTGTTGCTGGGCTGGACAGCTGACAGCTGTGC 780
QY 812 GACGGGACCGTGTGGCGGAACAGCGGCGCTGAGCTGTACCCCTTACGACGCCGCGAGC 871
DB 781 GACGGGACCGTGTGGCGGAACAGCGGCGCTGAGCTGTACCCCTTACGACGCCGGAACG 840
QY 872 GACAGGGGCTTCACTTCT 931
DB 841 GACAGGGGCTTCACTTCT 900
QY 932 GAGATAACCT 991
DB 901 GAGATAACCT 960
QY 992 GGCCTGCT 1051
DB 961 GGCCTGCT 1020
QY 1052 ATCCCT 1111
DB 1021 ATCCCT 1080
QY 1112 CCAGAAACCGCTGGAGTGCAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1171
DB 1081 CCAGAAACCGCTGGAGTGCAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1140
QY 1172 CACTGTGGGAGGCTCGGGACCAAGAGCAGGACTCGCTACGTCCTCGGCTCCAGCCCGCCAC 1231
DB 1141 CACTGTGGGAGGCTCGGGACCAAGAGCAGGACTCGCTACGTCCTCGGCTCCAGCCCGCCAC 1200
QY 1232 AACGGAGGCGCTGCGCGGCTCGAGAGGCTGAGTGGCTCCCTGATTAACCTCGCTC 1291
DB 1201 AACGGAGGCGCTGCGCGGCTCGAGAGGCTGAGTGGCTCCCTGATTAACCTCGCTC 1260
QY 1292 TAAGACACAGCCCGCAGCCCTGCGGCGCCCGCGAGGCAATGGGCTGTCTGGGGCTCTCT 1351
DB 1261 TAAGACACAGCCCGCAGCCCTGCGGCGCCCGCGAGGCAATGGGCTGTCTGGGGCTCTCT 1320
QY 1352 GTGCGAGGCTCATGCTGCGAGGCGCGAGGCGACAGGGGTTTTTTCGCGCTCTCTTGACCGC 1411
DB 1321 GTGCGAGGCTCATGCTGCGAGGCGCGAGGCGACAGGGGTTTTTTCGCGCTCTCTTGACCGC 1380
QY 1412 GGTGAGGCGCGCGCAGCAGCTCTCTGCTGAGGCGCTCTGCTGGCGCGGCGAGGCGCATTT 1471
DB 1381 GGTGAGGCGCGCGCAGCAGCTCTCTGCTGAGGCGCTCTGCTGGCGCGGCGAGGCGCATTT 1440

QY 1472 GGAACACGCTCCTCTTCCAACTTGTCTTTAGGGGCCCGGTGTCCCGTGTCT 1531
|||||
Db 1441 GGAACACGCTCCTCTTCCAACTTGTCTTTAGGGGCCCGGTGTCCCGTGTCT 1500
|||||
QY 1532 CTCAGCTCCTCCTCTCTCAGGATAAAGTCATCCCAAGGCTCCAGCTACTCTAAATTAT 1591
|||||
Db 1501 CTCAGCTCCTCCTCTCTCAGGATAAAGTCATCCCAAGGCTCCAGCTACTCTAAATTAT 1560
|||||
QY 1592 GTCCTCTTAAAGTTATTCCTCTCCAGGAGATGTCCTTCATCGTCCAGGGCCCTGGCT 1651
|||||
Db 1561 GTCCTCTTAAAGTTATTCCTCTCCAGGAGATGTCCTTCATCGTCCAGGGCCCTGGCT 1620
|||||
QY 1652 CCCAGCTGGTTCCAGATACCTCAGACCTGGTGTCTTAGGCTGTGTAGCCCACTCTCCC 1711
|||||
Db 1621 CCCAGCTGGTTCCAGATACCTCAGACCTGGTGTCTTAGGCTGTGTAGCCCACTCTCCC 1680
|||||
QY 1712 GAGGGGCGATCAAGGGGGGCACTTGAGAGTGTAATAAGGGCGGTTCGGGAAGCG 1771
|||||
Db 1681 GAGGGGCGATCAAGGGGGGCACTTGAGAGTGTAATAAGGGCGGTTCGGGAAGCG 1740
|||||
QY 1772 TCAGTGTTCCTCATGTTATGATCTCTCTCGGTTTGAATAAGACTATCTGTGTGCTC 1829
|||||
Db 1741 TCAGTGTTCCTCATGTTATGATCTCTCTCGGTTTGAATAAGACTATCTGTGTGCTC 1798
|||||
RESULT 9
AAF90566
ID AAF90566 standard; DNA; 1785 BP.
XX
AC AAF90566;
XX
DT 22-AUG-2001 (first entry)
XX
DE Human extracellular matrix protein RGL DNA.
XX
KW RGL; human; extracellular matrix protein; prostate cancer;
KW metastasis; tumour; benign prostatic hyperplasia; gene therapy;
KW diagnosis; antitumour; ds.
XX
OS Homo sapiens.
XX
FH Key
FT CDS 296..1294
FT /*tag= a
XX
PN WO200144291-A2.
XX
PD 21-JUN-2001.
XX
PF 15-DEC-2000; 2000WO-US33901.
XX
PR 16-DEC-1999; 99US-0172370.
PR 07-DEC-2000; 2000US-9966561.
XX
XX (SCHD) SCHERING AG.
XX
XX Harkins R, Parkes D, Parry G, Schneider DW, Steinbrecher R;
PI WPI; 2001-398128/42.
DR P-PSDB; AAB82472.
XX
PT Novel human extracellular matrix polypeptide, RGL, useful in research,
PT diagnosis and treatment of metastasis such as prostate cancer
XX Claim 8; Fig 1; 69pp; English.
XX
CC The present sequence is that of a polynucleotide, designated rgl,
CC encoding novel human extracellular matrix polypeptide RGL (see
CC AAB82472). The full-length coding sequence was deduced from a
CC clone identified from a database screening that was found in the
CC category of cell adhesion molecules and described as a homologue
CC of f-spondin. RGL is expressed in prostate tissue and may be

over-expressed in prostate tumours. It shows homology to a
superfamily of extracellular matrix proteins encoded by the
mindin/f-spondin genes. The invention provides human RGL
polypeptides, polynucleotides encoding them (especially encoding
amino acids 1-331, 21-331 or 27-331 of RGL), methods for
producing the polypeptides, expression vectors and genetically
engineered host cells for expression of the polypeptides. It
also provides methods for utilizing the polynucleotides and
polypeptides in research, diagnosis and therapeutic applications.
Thus, rgl polynucleotides can be used in the production of
recombinant proteins, in methods for assessing RGL expression
in cells, and in the development of ribozyme and antisense
oligonucleotides useful for administration e.g. to a human
patient for treatment of a disease such as prostate cancer or
benign prostatic hyperplasia, which is alleviated by decreasing
the level of RGL activity.
XX
SQ Sequence 1785 BP; 300 A; 614 C; 570 G; 301 T; 0 other;
Query Match 95.7%; Score 1761.2; DB 22; Length 1785;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1763; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 9 GGGGTGCGGCAGCACTGCGAGGGGAAGAGGGTGATCCGACCCGGGGAAGTCTCGTGGCA 68
|||||
Db 6 GGGGTGCGGCAGCACTGCGAGGGGAAGAGGGTGATCCGACCCGGGGAAGTCTCGTGGCA 65
|||||
QY 69 GGGCGAGTTGGGAAGCGGCAGCCCCCGCGCCCGCCGCGAGCCCTTCTCTCTTTCTCC 128
|||||
Db 66 GGGCGAGTTGGGAAGCGGCAGCCCCCGCGCCCGCCGCGAGCCCTTCTCTCTTTCTCC 125
|||||
QY 129 CAGCTCTATCTGCTCTCTGAGGCCAGGCCGTCGAGCATCGAAGACAGAGGAACT 188
|||||
Db 126 CAGCTCTATCTGCTCTCTGAGGCCAGGCCGTCGAGCATCGAAGACAGAGGAACT 185
|||||
QY 189 GGAGCTCATTTGGCGGCGCCGGGGCCCGCTTCGGGCTTAAATAGAGCTCCGGGCTCT 248
|||||
Db 186 GGAGCTCATTTGGCGGCGCCGGGGCCCGCTTCGGGCTTAAATAGAGCTCCGGGCTCT 245
|||||
QY 249 GGTGGGACCGGACCGCTGCGGCGCGGCTCCCGCTGCTCTCTCCGGGTGATGGAAGCC 308
|||||
Db 246 GGTGGGACCGGACCGCTGCGGCGCGGCTCCCGCTGCTCTCTCCGGGTGATGGAAGCC 305
|||||
QY 309 CCAGCCCGGCGCGCGCTGGGCAAGGCCCTCTGCGCTCTCTCTCTGCGGCTCTCGGCG 368
|||||
Db 306 CCAGCCCGGCGCGCGCTGGGCAAGGCCCTCTGCGCTCTCTCTCTGCGGCTCTCGGCG 365
|||||
QY 369 CCGCCGCGCAGCTCTTTGGGGGAGAGTCCATCTGTTCCGCGCAGAGCCCGCGGCAATACA 428
|||||
Db 366 CCGCCGCGCAGCTCTTTGGGGGAGAGTCCATCTGTTCCGCGCGAGCCCGCGGCAATACA 425
|||||
QY 429 GCATCACCTTCAGGGCAAGTGGAGCCAGAGCGGCTTCCCAAGCAGTACCCCTGTTC 488
|||||
Db 426 GCATCACCTTCAGGGCAAGTGGAGCCAGAGCGGCTTCCCAAGCAGTACCCCTGTTC 485
|||||
QY 489 GCGCCCTCGCAGTGTCTTCTGCTGCTGGGGCCCGCATAGCTCCGACTACAGCATGT 548
|||||
Db 486 GCGCCCTCGCAGTGTCTTCTGCTGCTGGGGCCCGCATAGCTCCGACTACAGCATGT 545
|||||
QY 549 GGAGGAAGAACCAAGTACGTACGTACGGGTGCGGCACTTTGCGGAGCCGCGGAGGCGCT 608
|||||
Db 546 GGAGGAAGAACCAAGTACGTACGTACGGGTGCGGCACTTTGCGGAGCCGCGGAGGCGCT 605
|||||
QY 609 GGGCGCTGATGAAGAGATCGAGGCGCGGGGAGCGGCTGCGAGCGTGCACGAGGTGT 668
|||||
Db 606 GGGCGCTGATGAAGAGATCGAGGCGCGGGGAGCGGCTGCGAGCGTGCACGAGGTGT 665
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QY 669 TTTGCGCGCCCGCGCTCCAGCGGCGCAGCGGAGCTGCGGCGGAGCTGGAGGTGCAGC 728
|||||
Db 666 TTTGCGCGCCCGCGCTCCAGCGGCGCAGCGGAGCTGCGGCGGAGCTGGAGGTGCAGC 725
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QY 729 GCAGGCACTCGTGTCTCTGTTGTGTGTGCGCATCTGCCAGCCCGGACTGGTGTCTGG 788
|||||

Db	726	GCAGGCAC	TCGC	GTCTCG	TTTGTG	TGCG	CATCG	TGCC	CAGCCCCG	CAC	TGTTG	CTGTGG	785			
Qy	789	GCCTGAC	AGACCT	TG	ACCTGT	GC	GACGGGG	ACCG	TGTG	CGGGAAC	AGCG	CGCGCTG	GAC	848		
Db	786	GCCTGAC	AGACCT	TG	ACCTGT	GC	GACGGGG	ACCG	TGTG	CGGGAAC	AGCG	CGCGCTG	GAC	845		
Qy	849	TGTAC	CCCTAC	AG	ACGGGG	AG	CAGGG	GGTTC	AC	CTTCT	CTCT	CCCC	AACTTC	GC	908	
Db	846	TGTAC	CCCTAC	AG	ACGGGG	AG	CAGGG	GGTTC	AC	CTTCT	CTCT	CCCC	AACTTC	GC	905	
Qy	509	CCATCCG	CAGGAC	CG	TG	ACCGAG	ATAAC	CTCT	CTCT	C	CC	CAG	CCACC	CG	968	
Db	906	CCATCCG	CAGGAC	CG	TG	ACCGAG	ATAAC	CTCT	CTCT	C	CC	CAG	CCACC	CG	965	
Qy	969	CCTTCTA	CTAC	CCCG	CG	CGCT	GA	AGGCC	CT	GC	CTCC	ATCG	CC	CAG	AGG	1028
Db	966	CCTTCTA	CTAC	CCCG	CG	CGCT	GA	AGGCC	CT	GC	CTCC	ATCG	CC	CAG	AGG	1025
Qy	1029	TGGC	CAGAGC	CC	CCAGG	GC	CTT	C	ATC	CTC	CC	CG	CC	CA	GT	1088
Db	1026	TGGC	CAGAGC	CC	CCAGG	GC	CTT	C	ATC	CTC	CC	CG	CC	CA	GT	1085
Qy	1089	AGATT	GT	AG	AC	GC	CTC	AG	TTCC	AG	AAAC	CG	CG	CT	GC	1148
Db	1086	AGATT	GT	AG	AC	GC	CTC	AG	TTCC	AG	AAAC	CG	CG	CT	GC	1145
Qy	1149	CGTCT	CGG	ACT	TG	TCG	GAG	GC	ACT	TG	GAG	GC	TCG	GAG	GC	1208
Db	1146	CGTCT	CGG	ACT	TG	TCG	GAG	GC	ACT	TG	GAG	GC	TCG	GAG	GC	1205
Qy	1209	ACGT	CCGG	TCC	AG	CCG	CC	CAAC	AG	GG	AG	CC	CTG	CC	CG	1268
Db	1206	ACGT	CCGG	TCC	AG	CCG	CC	CAAC	AG	GG	AG	CC	CTG	CC	CG	1265
Qy	1269	AGT	CG	CTC	CT	G	AT	ACT	CG	CT	TAAG	AC	CAG	CCG	CG	1328
Db	1266	AGT	CG	CTC	CT	G	AT	ACT	CG	CT	TAAG	AC	CAG	CCG	CG	1325
Qy	1329	GCCAT	GGG	TG	TCG	GG	GT	CT	CT	TG	C	AG	GG	CG	C	1388
Db	1326	GCCAT	GGG	TG	TCG	GG	GT	CT	CT	TG	C	AG	GG	CG	C	1385
Qy	1389	GGTTT	CG	CG	CT	CT	G	AT	CG	CG	TG	AG	CG	CG	CG	1448
Db	1386	GGTTT	CG	CG	CT	CT	G	AT	CG	CG	TG	AG	CG	CG	CG	1445
Qy	1449	CTCT	TG	TG	CG	CG	C	AG	GC	AT	TG	G	AA	AC	GC	1508
Db	1446	CTCT	TG	TG	CG	CG	C	AG	GC	AT	TG	G	AA	AC	GC	1505
Qy	1509	GGG	CCCC	CG	TG	CC	GT	CT	CT	C	T	C	AG	CC	T	1568
Db	1506	GGG	CCCC	CG	TG	CC	GT	CT	CT	C	T	C	AG	CC	T	1565
Qy	1569	AGG	CT	CC	AG	CT	ACT	TA	A	T	T	AT	G	T	CT	1628
Db	1566	AGG	CT	CC	AG	CT	ACT	TA	A	T	T	AT	G	T	CT	1625
Qy	1629	CTT	C	AT	G	T	C	C	AG	G	GC	T	G	G	T	1688
Db	1626	CTT	C	AT	G	T	C	AG	G	GC	T	G	G	T	C	1685
Qy	1689	GG	CT	G	T	G	T	C	AG	G	GC	CA	T	CC	AA	1748
Db	1686	GG	CT	G	T	G	T	C	AG	G	GC	CA	T	CC	AA	1745
Qy	1749	TAA	T	GGG	CG	G	T	T	CG	GA	AG	CG	CT	CA	1774	
Db	1746	TAA	T	GGG	CG	G	T	T	CG	GA	AG	CG	CT	CA	1771	

AAAF0567	standard; DNA; 1770 BP.
AAAF0567;	
22-AUG-2001	(first entry)
Human extracellular matrix protein RGL DNA.	
RGL1; extracellular matrix protein; prostate cancer;	
metastasis; tumour; benign prostatic hyperplasia; gene therapy;	
diagnosis; antitumour; ds.	
Homo sapiens.	
Key	Location/Qualifiers
CDS	296..1294
FT	/*tag= a
WO200144291-A2.	
21-JUN-2001.	
15-DEC-2000; 2000WO-US33901.	
16-DEC-1999; 99US-0172370.	
07-DEC-2000; 2000US-9966561.	
(SCHD) SCHERING AG.	
Harkins R, Parkes D, Parry G, Schneider DW, Steinbrecher R;	
WPI; 2001-398128/42.	
P-PSDB; AAB90567.	
Novel human extracellular matrix polypeptide, RGL, useful in research;	
diagnosis and treatment of metastasis such as prostate cancer -	
Disclosure; Fig 4; 69pp; English.	
The present sequence is that of a polynucleotide, designated rgl,	
encoding novel human extracellular matrix polypeptide RGL (see	
AA82472). The full-length coding sequence was deduced from a	
clone identified from a database screening that was found in the	
category of cell adhesion molecules and described as a homologue	
of f-spondin. RGL is expressed in prostate tissue and may be	
over-expressed in prostate tumours. It shows homology to a	
superfamily of extracellular matrix proteins encoded by the	
mindin/f-spondin genes. The invention provides human RGL	
polypeptides, polynucleotides encoding them (especially encoding	
amino acids 1-331, 21-331 or 27-331 of RGL), methods for	
producing the polypeptides, expression vectors and genetically	
engineered host cells for expression of the polypeptides. It	
also provides methods for utilizing the polynucleotides and	
polypeptides in research, diagnosis and therapeutic applications.	
Thus, rgl polynucleotides can be used in the production of	
recombinant proteins, in methods for assessing RGL expression	
in cells, and in the development of ribozyme and antisense	
oligonucleotides useful for administration e.g. to a human	
patient for treatment of a disease such as prostate cancer or	
benign prostatic hyperplasia, which is alleviated by decreasing	
the level of RGL activity.	
Sequence 1770 BP; 285 A; 614 C; 570 G; 301 T; 0 other;	

	Query Match	95.7%	Score 1760.2	DB 22	Length 1770
	Best Local Similarity	99.8%	Pred. No. 0		
	Matches 1762	Conservative	0	Mismatches	3
				Indels	0
				Gaps	0
y	9	GGGGTGGCGACACTGCGAGGGGAAGAGGGTGATCCGACCCGGGAAGTGGCTGGGCA	68		
b	6	GGGGTGGCGACACTGCGAGGGGAAGAGGGTGATCCGACCCGGGAAGTGGCTGGGCA	65		
	69	GGGCGAGTTGGGAAAGCGCAGCCCGCCGCCGCCGAGCCCTTCCTCTCTCTCTCC	128		

Db	66	GGGCGAGTTGGGAAAGCGGAGCCCGCCGCGCCGAGAGCCCTTCCTCCTTTCTCC	125
Qy	129	CAGCTCCTATCTCGCTCTCGCTGGAGGCGAGCCGTGCAGCATCGAAGCAGAGGAACT	188
Db	126	CAGCTCCTATCTCGCTCTCGCTGGAGGCGAGCCGTGCAGCATCGAAGCAGAGGAACT	185
Qy	189	GGAGCCTCATTTGGCCGCCCGGGGGCGCGCTTCGGGCTTAATAAGAGCTCCGGGCTCT	248
Db	186	GGAGCCTCATTTGGCCGCCCGGGGGCGCGCTTCGGGCTTAATAAGAGCTCCGGGCTCT	245
Qy	249	GGCTGGGACCCGACCGCTGCGCGCGCGCTCCCGTGTCTCTGCGGGTGATGGAATAAC	308
Db	246	GGCTGGGACCCGACCGCTGCGCGCGCGCTCCCGTGTCTCTGCGGGTGATGGAATAAC	305
Qy	309	CCAGCCCGCGCGCGCTTGGCAAGGCCCTCTGGCTCTCTCTCTGSCCACTCTCGGCG	368
Db	306	CCAGCCCGCGCGCGCTTGGCAAGGCCCTCTGGCTCTCTCTCTGSCCACTCTCGGCG	365
Qy	369	CCGCCGCCAGCCTCTTGGGGGAGAGTCCATCTGTTCGCCAGAGCCCCGGCCAAATACA	428
Db	366	CCGCCGCCAGCCTCTTGGGGGAGAGTCCATCTGTTCGCCAGAGCCCCGGCCAAATACA	425
Qy	429	GCATCACCCTTACGGGCAAGTGGAGCCAGCGCCTTCCCAAGCAGTACCCCTGTTC	488
Db	426	GCATCACCCTTACGGGCAAGTGGAGCCAGCGCCTTCCCAAGCAGTACCCCTGTTC	485
Qy	489	GCCCCCTGCGCAGTGGTCTTGCTCTGGGGCGCGCATAGCTCCGACTACAGCATGT	548
Db	486	GCCCCCTGCGCAGTGGTCTTGCTCTGGGGCGCGCATAGCTCCGACTACAGCATGT	545
Qy	549	GGAGGAAGAACCACTAGTCAGTAACGGGCTCGCGGACTTTTCGGAGCGCGCGAGCGCT	608
Db	546	GGAGGAAGAACCACTAGTCAGTAACGGGCTCGCGGACTTTTCGGAGCGCGCGAGCGCT	605
Qy	609	GGGGCTGATGAAGAGAGATCGAGGCGCGGGGGAGGCGTTCGAGAGCTGCACGAGTGT	668
Db	606	GGGGCTGATGAAGAGAGATCGAGGCGCGGGGGAGGCGTTCGAGAGCTGCACGAGTGT	665
Qy	669	TTTCGGGCGCCGCGTCCCGAGGGCACGGGCACAGCTGCGCGGAGCTGCAGCTGCAGC	728
Db	666	TTTCGGGCGCCGCGTCCCGAGGGCACGGGCACAGCTGCGCGGAGCTGCAGCTGCAGC	725
Qy	729	GCAGGCACCTCGCTGCTCGTTTGTGTGTCGCATCGTGCCAGCCCGGACTGGTTCGTGG	788
Db	726	GCAGGCACCTCGCTGCTCGTTTGTGTGTCGCATCGTGCCAGCCCGGACTGGTTCGTGG	785
Qy	789	CGCTGGACACCTTGACCTGTGCGACGGGGACCGTTTGGGGGACAGCGCGCGCTGGACC	848
Db	786	CGCTGGACACCTTGACCTGTGCGACGGGGACCGTTTGGGGGACAGCGCGCGCTGGACC	845
Qy	849	TGTACCCCTACAGCGCGGAGCGAGCGGCTTCACCTTCCTCCGCCCAACTTCGCCA	908
Db	846	TGTACCCCTACAGCGCGGAGCGAGCGGCTTCACCTTCCTCCGCCCAACTTCGCCA	905
Qy	909	CCATCCCGCAGACCGGTGACCGAGATAACCTCTCTCCAGCCACCGCGGCAACT	968
Db	906	CCATCCCGCAGACCGGTGACCGAGATAACCTCTCTCCAGCCACCGCGGCAACT	965
Qy	969	CCTTCTACTACCGCGGCTGAAGGCCCTGCCATCGCCAGGGTGACACTGTGCGGC	1028
Db	966	CCTTCTACTACCCACGGCTGAAGGCCCTGCCATCGCCAGGGTGACACTGTGCGGC	1025
Qy	1029	TGGACAGAGCCCCAGGGCTTCATCCCTCCCGCCCCAGTCTGCCAGCAGGACAAATG	1088
Db	1026	TGGACAGAGCCCCAGGGCTTCATCCCTCCCGCCCCAGTCTGCCAGCAGGACAAATG	1085
Qy	1089	AGATTGTAGACGGCTCAGTTCCAGAAACGCCCTGGACTGCGAGGTCTCCCTGTGGT	1148
Db	1086	AGATTGTAGACGGCTCAGTTCCAGAAACGCCCTGGACTGCGAGGTCTCCCTGTGGT	1145
Qy	1149	CGTCCTGGGACTGTGCGGAGGCCACTGTGTGGAGGCTCGGGACCAAGAGCAGACTCGCT	1208

Db	1146	CGTCTGGGGACTGTGCGGAGGCCACTGTGGGAGGCTCGGGACCAGAGCAGGACTCGCT	1205
QY	1209	ACGTCGGGTCCAGCCCGCAACACGGGAGCCCTCCGCCAGCTCGAAGAAGAGGCTG	1268
Db	1206	ACGTCGGGTCCAGCCCGCAACACGGGAGCCCTCCGCCAGCTCGAAGAAGAGGCTG	1265
QY	1269	AGTCGGTCCCTGATACTGGTCTAAAGACACAGAGCCCGCAGCCCTCGGGCCCCCGGA	1328
Db	1266	AGTCGGTCCCTGATACTGGTCTAAAGACACAGAGCCCGCAGCCCTCGGGCCCCCGGA	1325
QY	1329	GCCATGGGTGTCGGGGGCTCTGTGCAAGCTCATGCTCAGCGGGCGAGGGCACAGGG	1388
Db	1326	GCCATGGGTGTCGGGGGCTCTGTGCAAGCTCATGCTCAGCGGGCGAGGGCACAGGG	1385
QY	1389	GTTTTCGGCTGTCCTTCAGCCGGGTGAGCGCGCCGACCATCTCTGCACTGAAGGGCC	1448
Db	1386	GTTTTCGGCTGTCCTTCAGCCGGGTGAGCGCGCCGACCATCTCTGCACTGAAGGGCC	1445
QY	1449	CTCTGGTGGCGGCACGGGCATTTGGAAACAGGCTCCTCTTTTCCCAACCTTGTCTCTTA	1508
Db	1446	CTCTGGTGGCGGCACGGGCATTTGGAAACAGGCTCCTCTTTTCCCAACCTTGTCTCTTA	1505
QY	1509	GGGGCCCCGTGTCCTCTCTCAGCCTCTCTCTCTCGCAGAGATTAAGTCATCCCCA	1568
Db	1506	GGGGCCCCGTGTCCTCTCTCAGCCTCTCTCTCTCGCAGAGATTAAGTCATCCCCA	1565
QY	1569	AGGCTCCAGCTACTCTAAATATGTCTCCCTATAAGTTATGCTCTCAGAGATTGTC	1628
Db	1566	AGGCTCCAGCTACTCTAAATATGTCTCCCTATAAGTTATGCTCTCAGAGATTGTC	1625
QY	1629	CTTCATCGTCCAGGGGCTTGGCTCCACAGCTGGTTGCAGATACCTCAGACCTGGTCTCTA	1688
Db	1626	CTTCATCGTCCAGGGGCTTGGCTCCACAGCTGGTTGCAGATACCTCAGACCTGGTCTCTA	1685
QY	1689	GGCTGTGCTGAGCCACTCTCCCGAGGGCGCATCCAAGCGGGGGCCACTTGAGAAGTAA	1748
Db	1686	GGCTGTGCTGAGCCACTCTCCCGAGGGCGCATCCAAGCGGGGGCCACTTGAGAAGTAA	1745
QY	1749	TAAATGGGCGGTTTCGGAAGCGTC	1773
Db	1746	TAAATGGGCGGTTTCGGAAGCGTC	1770
RESULT 11			
AAD20094			
ID	AAD20094 standard; cDNA; 1779 BP.		
XX			
AC	AAD20094;		
XX			
DT	03-JAN-2002 (first entry)		
XX			
DE	Human NPG-1 cDNA.		
XX			
KW	Human; NPG-1; cytostatic; gene therapy; tumour; prostate cancer; LCS;		
KW	Linker Capture Subtraction; genetic alteration; nerve cell growth; ss.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	236..1228	
FT	/*tag= a		
FT	/product= "Human NPG-1 protein"		
XX			
PN	US6287777-B1.		
XX			
XX	11-SEP-2001.		
XX			
PF	10-AUG-1999;	99US-0371696.	
XX			
PR	10-MAY-1996;	96US-0644326.	
PR	11-FEB-1998;	98US-0022238.	
PA	(BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.		

QY 1801 CGTTTGAATAAAGACTATCTGTTGCTCAAAAAA 1840
AAC59794
|||||
Db 1737 CGTTTGAATAAAGATACTCTGTTGCTCAAAAAA 1776

RESULT 12
AAC59794
ID AAC59794 standard; DNA; 1718 BP.
XX AAC59794;

AC AAC59794;
XX
DT 26-JAN-2001 (first entry)
XX

DE Human secreted protein encoding DNA clone vp22 1.
XX

XX Secreted protein; human; autoimmune disorder; multiple sclerosis; ulcer;
KW systemic lupus erythematosus; rheumatoid arthritis; anaemia; stroke;
KW haematopoiesis regulation; tissue regrowth; wound healing; haemophilia;
KW Alzheimer's disease; Parkinson's disease; Shy-drager syndrome; cancer;
KW contraceptive; infection; growth inhibition; hyperproliferative disorder;
KW psoriasis; ds.
XX

OS Homo sapiens.
XX

XX WO200055375-A1.
PN

XX 21-SEP-2000.
PD

XX 17-MAR-2000; 2000WO-US07285.
PF

XX 17-MAR-1999; 99US-0124808.
PR

XX 17-MAR-1999; 99US-0124916.
PR

XX 17-AUG-1999; 99US-0149639.
PR

XX 01-OCT-1999; 99US-0157247.
PR

XX 29-NOV-1999; 99US-0167824.
PR

XX 15-FEB-2000; 2000US-0182711.
PR

XX (ALPH-) ALPHAGENE INC.
PA

XX Valenzuela D, Yuan O, Hoffman H, Hall J, Raplejo P;
PI
XX WPI; 2000-638211/61.
DR

XX P-PSDB; AAB34693.
DR

XX Novel proteins and polypeptides useful for the treatment of e.g
PT multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis,
PT cancer, Alzheimer's disease, Parkinson's disease, stroke, anemia and
PT ulcers -
PT
XX

XX Claim 22; Page 394-395; 493pp; English.
PS

XX This invention relates to 59 human secreted proteins and the nucleotide
CC sequences encoding them. Sequences AAC59788-C59846 and AAB34687-B34745
CC represent the proteins and their encoding nucleotide sequences, and
CC sequences AAB34746-B34771 represent fragments of the proteins. Probes
CC for the DNA sequences are represented by sequences AAC59847-C59596. The
CC proteins exhibit neuroprotective, dermatological, immunosuppressive,
CC antiinflammatory, antianemic, nootropic, antiparkinsonian,
CC cerebroprotective, haemostatic, vulnerrary, cytostatic, antipsoriatic,
CC antibacterial, virucide, and fungicide activity. The proteins and
CC nucleotide sequences are useful as nutritional sources or supplements
CC and in research. The proteins are useful for treating immune deficiency
CC and disorders, which may be genetic or resulting from infections,
CC autoimmune disorders such as multiple sclerosis, systemic lupus
CC erythematosus, rheumatoid arthritis, and for treating myeloid or lymphoid
CC cell deficiencies such as anaemias by regulating haematopoiesis. The
CC proteins are also useful in compositions for bone, cartilage, tendon,
CC ligament and/or nerve tissue growth or regeneration, for wound healing,
CC tissue repair and replacement and in the treatment of wounds, incisions
CC and ulcers. Other uses include in the treatment of central and
CC peripheral nervous system and neuropathies such as Alzheimer's and
CC Parkinson's diseases and Shy-Drager syndrome, and mechanical and

CC traumatic disorders, such as spinal cord disorders, head trauma and
CC stroke. The proteins may also be used as a contraceptive, and for
CC treating coagulation disorders such as haemophilias. The protein and
CC nucleotide sequences with cadherin activity are useful for treating
CC cancer. Other uses for the protein include for inhibiting the growth,
CC infection or function of, or killing, infectious agents such as bacteria,
CC virus, fungi and other parasites, for effecting biorhythms or cardiac
CC such as height, weight, hair colour, effecting biorhythms or cardiac
CC cycles or rhythms, effecting metabolism, catabolism, anabolism,
CC processing, utilization, storage or elimination of dietary fat, lipid,
CC protein, carbohydrate, vitamins, minerals, cofactors, effecting
CC behavioural characteristics, providing analgesic effects and for treating
CC hyperproliferative disorders such as psoriasis.
XX

SQ Sequence 1718 BP; 297 A; 579 C; 535 G; 307 T; 0 other;

Query Match 91.6%; Score 1686.2; DB 21; Length 1718;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1699; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 138 TCTGCTCTCGCTGGAGGCCAGGCCCTGCAGCATCGAAGACAGGAGAACTGGAGCCTCA 197
Db |||||||
2 TCTGCTCTCGCTGGAGGCCAGGCCCTGCAGCATCGAAGACAGGAGAACTGGAGCCTCA 61

QY 198 TTGGCCGCCGCCGCCGCTCGGGCTTAAATAGAGCTCCCGGCTCTGGCTGGGAC 257
|||||
Db 62 TTGGCCGCCGCCGCCGCTCGGGCTTAAATAGAGCTCCCGGCTCTGGCTGGGAC 121

QY 258 CCGACGCTGCGCGCGCGCTCCCGCTGCTCTGCGGGTGATGGAACACCCAGCCCGG 317
|||||
Db 122 CCGACGCTGCGCGCGCGCTCCCGCTGCTCTGCGGGTGATGGAACACCCAGCCCGG 181

QY 318 CCGCGCCCTTGGCAAGGCCCTCTGCGCTCTCTCTGCGGCTCTGCGGCGCGCGGCC 377
|||||
Db 182 CCGCGCCCTTGGCAAGGCCCTCTGCGCTCTCTCTGCGGCTCTGCGGCGCGCGGCC 241

QY 378 AGCCTCTTGGGGAGAGTCCATCTGTTCCGCCAGAGCCCGGCCAAATACAGCATCACCT 437
|||||
Db 242 AGCCTCTTGGGGAGAGTCCATCTGTTCCGCCAGAGCCCGGCCAAATACAGCATCACCT 301

QY 438 TCACGGCAAGTGGAGCCAGAGCGGCTTCCCAAGCAGTACCCCTGTTCCGCGCCCTCG 497
|||||
Db 302 TCACGGCAAGTGGAGCCAGAGCGG -CTTCCCAAGCAGTACCCCTGTTCCGCGCCCTCG 360

QY 498 CCGAGTGGTCTTCGCTGCTGGGGCGCGCATAGCTCCGACTACAGCATGTGGAGGAAGA 557
|||||
Db 361 CCGAGTGGTCTTCGCTGCTGGGGCGCGCATAGCTCCGACTACAGCATGTGGAGGAAGA 420

QY 558 ACCAGTACCTCAGTAACGGGCTGCGGCTTTTCCGAGCGCGGCGAGGCTTGGGCGCTGA 617
|||||
Db 421 ACCAGTACCTCAGTAACGGGCTGCGGCTTTTCCGAGCGCGGCGAGGCTTGGGCGCTGA 480

QY 618 TGAAGGAGATCGAGGCGCGGGGAGGCGCTGCAGAGCGTGCACAGAGTGTGTTTCGGCGC 677
|||||
Db 481 TGAAGGAGATCGAGGCGCGGGGAGGCGCTGCAGAGCGTGCACAGCGTGTGTTTCGGCGC 540

QY 678 CCGCGCTTCCAGCGCCAGCGCTGCGGAGCTGCGGAGTGGAGGTGCAGCGCAGGCACT 737
|||||
Db 541 CCGCGCTTCCAGCGCCAGCGCTGCGGAGCTGCGGAGTGGAGGTGCAGCGCAGGCACT 600

QY 738 CGCTGCTCTGTTGTTGCTGCGCATCGTCCAGCCCGGCTGTTCTGTTGGGCGTGGACA 797
|||||
Db 601 CGCTGCTCTGTTGTTGTTGCTGCGCATCGTCCAGCCCGGCTGTTCTGTTGGGCGTGGACA 660

QY 798 GCCTGGACCTGTGCGACGGGGACCGGTTGGCGGGAACAGCGCGCTGGACCTGTACCCCT 857
|||||
Db 661 GCCTGGACCTGTGCGACGGGGACCGGTTGGCGGGAACAGCGCGCTGGACCTGTACCCCT 720

QY 858 AGACGCCGGGACGAGCGGCTTACCTTCTCCCAACTTCGCCACCATCCCGC 917
|||||
Db 721 AGACGCCGGGACGAGCGGCTTACCTTCTCCCAACTTCGCCACCATCCCGC 780

QY 918 AGSACACGCTGACCGAGATAACGCTCTCTCCAGCCACCGCGCAACTCTCTTACT 977

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Db 781 AGGACACGGTGAACGAGATTAACGTCCTCTCCACACACCGGCAACTCCTTCTACT 840
QY ACCCGCGGTGAAGGCGCTTCCATCCGACAGGCTGACACTGCTGCGCTCGACAG 1037
Db 841 ACCCGCGGTGAAGGCGCTTCCATCCGACAGGCTGACACTGCTGCGCTCGACAG 900
QY 1038 GCGCCAGGCGCTTTCATCCCTCCCGCCCCAGTCTGCCCCAGCAGGACAATGAGATTGTAG 1097
Db 901 GCGCCAGGCGCTTTCATCCCTCCCGCCCCAGTCTGCCCCAGCAGGACAATGAGATTGTAG 960
QY 1098 ACAGCGCTTCAGTTCCAGAAACCGCTGGACTGCGAGTCTCCCTGCTGCTGCTGCTG 1157
Db 961 ACAGCGCTTCAGTTCCAGAAACCGCTGGACTGCGAGTCTCCCTGCTGCTGCTGCTG 1020
QY 1158 GACTGTGCGGAGGCGCTGCTGCGAGGCTCGGACCAAGAGCAGGAGTCTGCTAGTCCGG 1217
Db 1021 GACTGTGCGGAGGCGCTGCTGCGAGGCTCGGACCAAGAGCAGGAGTCTGCTAGTCCGG 1080
QY 1218 TCCAGCGCCCAACACGAGGCGCTGCTGCGAGGCTCGAAGAAGAGTCTGCTGCTGCTG 1277
Db 1081 TCCAGCGCCCAACACGAGGCGCTGCTGCGAGGCTCGAAGAAGAGTCTGCTGCTGCTG 1140
QY 1278 CTGATTAATGCTTAAGACAGAGCGCCGCGAGCCCTGCGGCGCCCGCGAGGAGTGGGG 1337
Db 1141 CTGATTAATGCTTAAGACAGAGCGCCGCGAGCCCTGCGGCGCCCGCGAGGAGTGGGG 1200
QY 1338 TGTGCGGGGCTCTCTGTCAGGCTCATGCTGTCAGGCGCGGAGGACACAGGGTTCGCG 1397
Db 1201 TGTGCGGGGCTCTCTGTCAGGCTCATGCTGTCAGGCGCGGAGGACACAGGGTTCGCG 1260
QY 1398 CTGCTCTGACCGCGTGAAGCGCGCGCCGACCATCTCTGCTGCTGCTGCTGCTGCTG 1457
Db 1261 CTGCTCTGACCGCGTGAAGCGCGCGCCGACCATCTCTGCTGCTGCTGCTGCTGCTG 1320
QY 1458 CCGGACGCGCATTGGAAACAGGCTCTCTCTTTCACACCTTCTTTCAGGCGCCCG 1517
Db 1321 CCGGACGCGCATTGGAAACAGGCTCTCTCTTTCACACCTTCTTTCAGGCGCCCG 1380
QY 1518 GTGTCGCGCTGCTCTGTCAGGCTCTCTCTCTGTCAGGATAAAGTCTATCCCAAGGCTCCAG 1577
Db 1381 GTGTCGCGCTGCTCTGTCAGGCTCTCTCTCTGTCAGGATAAAGTCTATCCCAAGGCTCCAG 1440
QY 1578 CTACTCTAAATATGCTCTCTTATAGTTATTTGCTGCTCCAGGAGATGCTCTTCTATCTG 1637
Db 1441 CTACTCTAAATATGCTCTCTTATAGTTATTTGCTGCTCCAGGAGATGCTCTTCTATCTG 1500
QY 1638 CCAGGCGCGCTGCTCTCCAGGCTGCTTGCAGATACCTCAGACCTGGTCTAGGCTGCTG 1697
Db 1501 CCAGGCGCGCTGCTCTCCAGGCTGCTTGCAGATACCTCAGACCTGGTCTAGGCTGCTG 1560
QY 1698 GAGCCCACTCTCCCGAGGCGCATCCCAAGCGGGGCGACTTGAGAGATGCAATAAATGGGG 1757
Db 1561 GAGCCCACTCTCCCGAGGCGCATCCCAAGCGGGGCGACTTGAGAGATGCAATAAATGGGG 1620
QY 1758 CGGTTTCGGAAGCGTCAGTGTGTTTCCATGTTATGATCTCTGCGGTTTGAATAAAGACTA 1817
Db 1621 CGGTTTCGGAAGCGTCAGTGTGTTTCCATGTTATGATCTCTGCGGTTTGAATAAAGACTA 1680
QY 1818 TCTCTGTTGCTCAAAAAA 1840
Db 1681 TCTCTGTTGCTCACAAAAA 1703
```

RESULT 13
AAH34981
ID AAH34981 standard; cDNA; 1848 BP.
XX
AC AAH34981;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen encoding cDNA SEQ ID NO:2063.

```
XX Human; colon cancer; colon cancer antigen; diagnosis; detection;  
KW colorectal carcinoma; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO2001122920-A2.  
XX  
PD 05-APR-2001.  
XX  
PF 28-SEP-2000; 2000WO-US26524.  
XX  
PR 29-SEP-1999; 99US-0157137.  
PR 03-NOV-1999; 99US-0163280.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Ruben SM, Barash SC, Birse CE, Rosen CA;  
XX  
DR WPI; 2001-235357/24.  
DR P-PSDB; AAG75576.  
XX  
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,  
XX useful for preventing, diagnosing and/or treating colorectal cancers -  
XX  
PS Claim 1; Page 3549; 9803pp; English.  
XX  
CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon  
CC cancer-associated nucleic acid molecules (N) and proteins (P), where  
CC the proteins are collectively known as colon cancer antigens. The colon  
CC cancer antigens have cytostatic activity and can be used in gene  
CC therapy and vaccine production. N and P may be used in the prevention,  
CC diagnosis and treatment of diseases associated with inappropriate P  
CC expression. For example, N and P may be used to treat disorders  
CC associated with decreased expression by rectifying mutations or deletions  
CC in a patient's genome that affect the activity of P by expressing  
CC inactive proteins or to supplement the patients own production of P.  
CC Additionally, N may be used to produce the colon cancer-associated Ps,  
CC by inserting the nucleic acids into a host cell and culturing the cell  
CC to express the proteins. N and P can be used in the prevention, diagnosis  
CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204  
CC and AAB7789 represent sequences used in the exemplification of the  
CC present invention.  
CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were  
CC missing at time of publication, meaning no sequences are present for  
CC SEQ ID NO:1027 to 1052, 7921 and 7922.
```

```
XX  
SQ Sequence 1848 BP; 324 A; 601 C; 578 G; 340 T; 5 other;  
  
Query Match 91.3%; Score 1680.8; DB 22; Length 1848;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1679; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
  
QY 158 AGCGCGTCGAGCATCGAAGACAGAGGAGAACTGGAGCCTATTGGCGCGCGCGCGCG 217  
Db 133 AGCGCGTCGAGCATCGAAGACAGAGGAGAACTGGAGCCTATTGGCGCGCGCGCGCG 192  
QY 218 GCCTCGGGCTTAAATAGGAGCTCCGGGCTCTGGTGGGACCCGACCGCTGCGCGCGCG 277  
Db 193 GCCTCGGGCTTAAATAGGAGCTCCGGGCTCTGGTGGGACCCGACCGCTGCGCGCGCG 252  
QY 278 TCCCGCTGCTCTGCGGGGTGATGGAACACCCAGCGCGCGCGCGCGCGCGCGCGCG 337  
Db 253 TCCCGCTGCTCTGCGGGGTGATGGAACACCCAGCGCGCGCGCGCGCGCGCGCGCG 312  
QY 338 CTCTGGGCTCTCTGCGGCACTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 397  
Db 313 CTCTGGGCTCTCTGCGGCACTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 372  
QY 398 ATCTGTTCGCGCAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 457  
Db 373 ATCTGTTCGCGCAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 432
```

QY 458 ACGGCTTCCCAAGCAGTACCCCTGTGTTCCGCCGCCCTGCGCAGTGTCTTCGCTGCTG 517
|||||
Db 433 ACGGCTTCCCAAGCAGTACCCCTGTGTTCCGCCGCCCTGCGCAGTGTCTTCGCTGCTG 492
|||||
QY 518 GGGGGCGGCATAGCTCCGACTACAGCATGTGAGAGAAACACAGTACGTACAGTACCGG 577
|||||
Db 493 GGGGGCGGCATAGCTCCGACTACAGCATGTGAGAGAAACACAGTACGTACAGTACCGG 552
|||||
QY 578 CTGCGCGACTTTGCGGAGCGCGGAGGCTGCGGCGCTGATGAAGAGAGATCCAGCGCGG 637
|||||
Db 553 CTGCGCGACTTTGCGGAGCGCGGAGGCTGCGGCGCTGATGAAGAGAGATCCAGCGCGG 612
|||||
QY 638 GGGGAGCGCTCAGAGCGCTGACAGAGTGTGTTTCGGCGCCCGCGTCCCGACGCGCAC 697
|||||
Db 613 GGGGAGCGCTCAGAGCGCTGACAGAGTGTGTTTCGGCGCCCGCGTCCCGACGCGCAC 672
|||||
QY 698 GGGGAGCGCTCGGAGAGTGTGAGGTGACAGCGACGACTCGTGTCTCGTTTGTGTTG 757
|||||
Db 673 GGGGAGCGCTCGGAGAGTGTGAGGTGACAGCGACGACTCGTGTCTCGTTTGTGTTG 732
|||||
QY 758 CGCATCGTCCCGACGCCCGACTGTTCTGTTGGCGTGGACAGCCTGGACCTGTGCGACGG 817
|||||
Db 733 CGCATCGTCCCGACGCCCGACTGTTCTGTTGGCGTGGACAGCCTGGACCTGTGCGACGG 792
|||||
QY 818 GACCCTTGGCGGAAACAGCGCGGCTGGACCTGTACCCCTAGCAGCCCGGACGCGACAGC 877
|||||
Db 793 GACCCTTGGCGGAAACAGCGCGGCTGGACCTGTACCCCTAGCAGCCCGGACGCGACAGC 852
|||||
QY 878 GGGTTACCTTCTCTCCCGCCCACTTTCGCGACCATCCCGCAGGACACGGTGCACGAGATA 937
|||||
Db 853 GGGTTACCTTCTCTCCCGCCCACTTTCGCGACCATCCCGCAGGACACGGTGCACGAGATA 912
|||||
QY 938 AGCTCTCTCTCTCCAGCACCAGCGCACTCTCTTACTACCGCGGCTGAAGCCCTG 997
|||||
Db 913 AGCTCTCTCTCTCCAGCACCAGCGCACTCTCTTACTACCGCGGCTGAAGCCCTG 972
|||||
QY 998 CTCTCCATCCCGAGGTGACACTGTGCGGCTGCGACAGAGCCCGAGGCGCTTCATCCCT 1057
|||||
Db 973 CTCTCCATCCCGAGGTGACACTGTGCGGCTGCGACAGAGCCCGAGGCGCTTCATCCCT 1032
|||||
QY 1058 CCGGCCCAAGTCTGCGCCAGCAGGCAATGATGTAGACAGCGCCTCAGTTCCAGAA 1117
|||||
Db 1033 CCGGCCCAAGTCTGCGCCAGCAGGCAATGATGTAGACAGCGCCTCAGTTCCAGAA 1092
|||||
QY 1118 AGCGCGCTGAGTGGAGTCTCCCTGTGCTGTGCTGCGGAGTGTGCGAGGCGCACTGT 1177
|||||
Db 1093 AGCGCGCTGAGTGGAGTCTCCCTGTGCTGTGCTGCGGAGTGTGCGGAGGCGCACTGT 1152
|||||
QY 1178 GGGAGGCTCGGACCAAGACAGGACTCGCTACGTCGCGGTCCAGCCCGCCCAACACGGG 1237
|||||
Db 1153 GGGAGGCTCGGACCAAGACAGGACTCGCTACGTCGCGGTCCAGCCCGCCCAACACGGG 1212
|||||
QY 1238 AGCCCTGCCCCAGTCTCGAAGAGAGGCTGAGTGGTCCCTGATTAACGTGCGTCTAAGAC 1297
|||||
Db 1213 AGCCCTGCCCCAGTCTCGAAGAGAGGCTGAGTGGTCCCTGATTAACGTGCGTCTAAGAC 1272
|||||
QY 1298 CAGAGCCCGCAGCCCTCGGCGCCCGCCAGCCATGCGGCTGTGCGGCGCTCTGTCAG 1357
|||||
Db 1273 CAGAGCCCGCAGCCCTCGGCGCCCGCCAGCCATGCGGCTGTGCGGCGCTCTGTCAG 1332
|||||
QY 1358 GCTCATGTGCGAGCGCGGACAGGCGGTTTCGCGCTGCTCCTACCGCGCGGTGAG 1417
|||||
Db 1333 GCTCATGTGCGAGCGCGGACAGGCGGTTTCGCGCTGCTCCTACCGCGGTGAG 1392
|||||
QY 1418 GCGGCGCCGACCATCTCTGCACTGAAGGCGCCTCTGTGTGGCGCGCACGGGCAATTGGGAA 1477
|||||
Db 1393 GCGGCGCCGACCATCTCTGCACTGAAGGCGCCTCTGTGTGGCGCGCACGGGCAATTGGGAA 1452
|||||
QY 1478 CAGCCTCTCTTCCCAACCTGCTCTTAGGGGCCCGCGTCCCGTCTGCTCAGC 1537
|||||
Db 1453 CAGCCTCTCTTCCCAACCTGCTCTTAGGGGCCCGCGTCCCGTCTGCTCAGC 1512
|||||
QY 1538 CTCCTCTCTCGAGGATAAAGTTCATCCCAAGGCTCCAGCTACTCTAAATATTGCTCC 1597
|||||

Db 1513 CTCCTCTCTCGAGGATAAAGTTCATCCCAAGGCTCCAGCTACTCTAAATATTGCTCC 1572
|||||
QY 1598 TTATAAGTTATTGCTGCTCCAGGAGATTGCTCTTATCTGTCAGGGGCTGGCTCCACG 1657
|||||
Db 1573 TTATAAGTTATTGCTGCTCCAGGAGATTGCTCTTATCTGTCAGGGGCTGGCTCCACG 1632
|||||
QY 1658 TCGTTGCAGATACCTCAGACCTGGTCTCTAGGCTGCTGAGCCACACTCTCCCGAGGGC 1717
|||||
Db 1633 TCGTTGCAGATACCTCAGACCTGGTCTCTAGGCTGCTGAGCCACACTCTCCCGAGGGC 1692
|||||
QY 1718 GCATCAAGCGGGGCCACTTGAGAAAGTGAATAAATGGGCGGTTTCGGAAGCGTCAGTG 1777
|||||
Db 1693 GCATCAAGCGGGGCCACTTGAGAAAGTGAATAAATGGGCGGTTTCGGAAGCGTCAGTG 1752
|||||
QY 1778 TTTCCATGTTATGGATCTCTCTGCGTTTGAATAAAGACTATCTCTGCTCAAAAAA 1837
|||||
Db 1753 TTTCCATGTTATGGATCTCTCTGCGTTTGAATAAAGACTATCTCTGCTCAAAAAA 1812
|||||
QY 1838 AAA 1840
|||||
Db 1813 AAA 1815
|||||
RESULT 14
AAK94182
ID AAK94182 standard; cDNA; 1669 BP.
XX
AC AAK94182;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human full-length cDNA, SEQ ID NO: 2726.
XX
KW Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
XX
OS Homo sapiens.
XX
PN EP1130094-A2.
XX
PD 05-SEP-2001.
XX
PF 07-JUL-2000; 2000EP-0114089.
XX
PR 08-JUL-1999; 99JP-0194486.
PR 11-JAN-2000; 2000JP-0118774.
PR 02-MAY-2000; 2000JP-0183765.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
DR WPI; 2001-524255/58.
DR P-PSDB; AAM93266.
XX
PT 830 Primers useful for synthesizing full length cDNA clones and their
PT use in genetic manipulation -
XX
PS Claim 8; SEQ ID NO 2726; 1380pp + sequence listing; English.
XX
CC The invention relates to primers for synthesising full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been
CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
CC molecules have been determined. Primers for synthesising the full length
CC cDNA are useful for clarifying the function of the protein encoded by
CC the cDNA. The full length clones were obtained by construction of full
CC length enriched cDNA libraries that were synthesised by the oligo-capping
CC method. The primers enable the production of the full length cDNA easily
CC without any special methods. The present sequence is a full length
CC human cDNA of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in CD-ROM format directly from EPO.

XX	Sequence 1669 BP; 273 A; 570 C; 525 G; 301 T; 0 other;	
SQ		
	Query Match 90.6%; Score 1666.4; DB 22; Length 1669;	
	Best Local Similarity 99.9%; Pred. No. 0;	
	Matches 1667; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	163 GTGAGCATCGAAGACAGGAGGAACTGGAGCCTCATTTGGCCGCGCGGCGCGCCCTC 222	
Db	1 GTGAGCATCGAAGACAGGAGGAACTGGAGCCTCATTTGGCCGCGCGGCGCGCCCTC 60	
QY	223 GGCTTTAAATAGAGAGTCCGGGCTCTGGCTGGAGACCGACCGTCCGGCCGGGCTCCCG 282	
Db	1 GGCTTTAAATAGAGAGTCCGGGCTCTGGCTGGAGACCGACCGTCCGGCCGGGCTCCCG 120	
QY	283 CTGCTCTCGCGGGTGATGAAACCCAGCCGCGCGCCCTGGGCAAGGCCCTCTG 342	
Db	121 CTGCTCTCGCGGGTGATGAAACCCAGCCGCGCGCCCTGGGCAAGGCCCTCTG 180	
QY	343 CGCTCTCTCTGGCCACTCTCGGCGCGCGCGCCAGCCCTCTTTGGGGAGAGTCCATCTG 402	
Db	181 CGCTCTCTCTGGCCACTCTCGGCGCGCGCGCCAGCCCTCTTTGGGGAGAGTCCATCTG 240	
QY	403 TTCGCGCAGAGCCCGGCCAAATACAGCATCAGCTTACGCGGCAAGTGAGCCAGAGCGC 462	
Db	241 TTCGCGCAGAGCCCGGCCAAATACAGCATCAGCTTACGCGGCAAGTGAGCCAGAGCGC 300	
QY	463 CTTCGCCAAGCAGTACCCCTGTTCGCCGCCCTGCGGCAAGTGCTCTGCTGGGGC 522	
Db	301 CTTCGCCAAGCAGTACCCCTGTTCGCCGCCCTGCGGCAAGTGCTCTGCTGGGGC 360	
QY	523 CGGCGATAGTCGAGTACAGCATGAGGAGGAGAACAGTACGTCAGTAACGGGCTGCG 582	
Db	361 CGGCGATAGTCGAGTACAGCATGAGGAGGAGAACAGTACGTCAGTAACGGGCTGCG 420	
QY	583 CGACTTTGCGGAGCGCGGAGCCCTGGCGCTGATGAGGAGATCGAGCGCGCGGGGA 642	
Db	421 CGACTTTGCGGAGCGCGGAGCCCTGGCGCTGATGAGGAGATCGAGCGCGCGGGGA 480	
QY	643 GCGCTGCAAGAGCGTCAGAGGTGTTTCGGCGCGCGCGCTCCCGACCGGCA 702	
Db	481 GCGCTGCAAGAGCGTCAGAGGTGTTTCGGCGCGCGCGCTCCCGACCGGCA 540	
QY	703 GAGTCGCGGAGCTGGAGGTGACGCGCAGGCACTCGCTGCTGTTGTTGGTGCAT 762	
Db	541 GAGTCGCGGAGCTGGAGGTGACGCGCAGGCACTCGCTGCTGTTGTTGGTGCAT 600	
QY	763 CGTGCCCGCGCGGCTGTTGTTGGCGGTGACAGCCCTGGAGCGGCGGACCG 822	
Db	601 CGTGCCCGCGCGGCTGTTGTTGGCGGTGACAGCCCTGGAGCGGCGGACCG 660	
QY	823 TTGGCGGGAACAGGCGCGCTGGACCTGTACCCCTACGACCGCGGACGACGCGGCTT 882	
Db	661 TTGGCGGGAACAGGCGCGCTGGACCTGTACCCCTACGACCGCGGACGACGCGGCTT 720	
QY	883 CACCTTCTCTCCCGCACTTCGCCACCATCCGCGAGGACAGCGGTGACCGAGATAACGTC 942	
Db	721 CACCTTCTCTCCCGCACTTCGCCACCATCCGCGAGGACAGCGGTGACCGAGATAACGTC 780	
QY	943 CTCCTCTCCAGGACCGCGCACTCTCTTACTACCGCGGCTGAAGGCCCTGCTCC 1002	
Db	781 CTCCTCTCCAGGACCGCGCACTCTCTTACTACCGCGGCTGAAGGCCCTGCTCC 840	
QY	1003 CATCGCGAGGTGACACTGTCGGCTGCGACAGAGCCCGCGGCTTATCCCTCCCGC 1062	
Db	841 CATCGCGAGGTGACACTGTCGGCTGCGACAGAGCCCGCGGCTTATCCCTCCCGC 900	
QY	1063 CCCAGTCTCCCGACAGGGAATGAGATGTGTAGACAGCGCTCAGTTCCAGAACGCC 1122	
Db	901 CCCAGTCTCCCGACAGGGAATGAGATGTGTAGACAGCGCTCAGTTCCAGAACGCC 960	
QY	1123 GCTGGACTCGGAGGTCTCCCTGCTGCTGCTGGGACTGTGGGAGGACCTGTGGGAG 1182	

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QY	1183 GCTCGGACCAAGACGAGGACTCGCTACGTCGCGGTCCAGCCGCCCAACAACGGAGCCC 1242	
Db	1021 GCTCGGACCAAGACGAGGACTCGCTACGTCGCGGTCCAGCCGCCCAACAACGGAGCCC 1080	
QY	1243 CTGCCCGAGCTCGAAGAAAGAGSCTGAGTGCCTGATTAAGTGCCTTAAGACAGAG 1302	
Db	1081 CTGCCCGAGCTCGAAGAAAGAGSCTGAGTGCCTGATTAAGTGCCTTAAGACAGAG 1140	
QY	1303 CCGCGAGCCCTGGGCGCCCGGAGCATGGGGTGTGCGGGGCTCTGTGAGGCTCA 1362	
Db	1141 CCGCGAGCCCTGGGCGCCCGGAGCATGGGGTGTGCGGGGCTCTGTGAGGCTCA 1200	
QY	1363 TGTGTCAGCGCGCGGACAGGAGGCTTTCGCGCTGCTCTGACCGGGTGTGAGCGCG 1422	
Db	1201 TGTGTCAGCGCGCGGACAGGAGGCTTTCGCGCTGCTCTGACCGGGTGTGAGCGCG 1260	
QY	1423 GCGGACCATCTCTGCACTGAAGGGCCCTCTGTGTGGCGGACGCGGATTTGGGAAACAGCC 1482	
Db	1261 GCGGACCATCTCTGCACTGAAGGGCCCTCTGTGTGGCGGACGCGGATTTGGGAAACAGCC 1320	
QY	1483 TCCTCTCTTCCCAACCTTCTTTCAGGGGCGCGGCTCTGCTCTGCTCTGAGCCCTCT 1542	
Db	1321 TCCTCTCTTCCCAACCTTCTTTCAGGGGCGCGGCTCTGCTCTGCTCTGAGCCCTCT 1380	
QY	1543 CTCTCTGCAAGGATAAAGTCAATCCCAAGGCTCCAGCTACTCTAAATATGTCTCTTATA 1602	
Db	1381 CTCTCTGCAAGGATAAAGTCAATCCCAAGGCTCCAGCTACTCTAAATATGTCTCTTATA 1440	
QY	1603 AGTATTGTGCTCCAGGAGATTGCTTTCATGTCACGAGGCGCTGGCTCCACGCTGGTT 1662	
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QY	1663 GCAGATACCTCAGACCTGCTGCTAGGCTGTGCTGAGCCCACTCTCCGAGGGCCATC 1722	
Db	1501 GCAGATACCTCAGACCTGCTGCTAGGCTGTGCTGAGCCCACTCTCCGAGGGCCATC 1560	
QY	1723 CAAGCGGGGCGCACCTTGAGAAGTGAATAAATGGGCGGTTTCGGAAGCGTCACTGTTTC 1782	
Db	1561 CAAGCGGGGCGCACCTTGAGAAGTGAATAAATGGGCGGTTTCGGAAGCGTCACTGTTTC 1620	
QY	1783 ATGTTATGATCTCTCTGCGTTTGAATAAAGACTATCTCTGTTGCTCA 1830	
Db	1621 ATGTTATGATCTCTCTGCGTTTGAATAAAGACTATCTCTGTTGCTCA 1668	
RESULT 15		
AAV63241		
ID	AAV63241 standard; cdNA; 1607 BP.	
XX		
AC	AAV63241;	
XX		
DT	21-JAN-1999 (first entry)	
XX		
DE	cdNA encoding an adhesion-modulating protein zsig25.	
XX		
KW	zsig25; adhesion-modulating protein; prostate cell; prostatic carcinoma;	
KW	B-cell cancer; infertility; Wolf-Hirschhorn syndrome;	
KW	chromosome 4 (p16.3); ss.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	40..1035
FT		/*tag= a
FT		/product= zsig25
XX		
PN	W09845442-A2.	
XX		
PD	15-OCT-1998.	
XX		
PF	10-APR-1998;	98WO-US07117.


```
XX 11-JUN-1997; 97US-0049288.
PR 10-APR-1997; 97US-0043421.
XX (ZYMO ) ZYMOGENETICS INC.
PA Sheppard PO;
XX PI
XX WIPI: 1998-557522/47.
DR P-PSDB; AAW70589.
XX
PT New zsig25 protein and related nucleic acid, fusion proteins,
PT vectors, transformed cells - and antibodies, involved in modulation
PT of adhesion, used for diagnosis and treatment of prostatic and
PT B-cell tumours, stimulation of haematopoietic cells, treatment of
PT immune deficiency etc.
XX
PS Claim 40; Pages 108-110; 161pp; English.
XX
CC The present sequence encodes a protein designated zsig25. The zsig25
CC protein is an adhesion-modulating protein expressed at very high level
CC in prostate cells. The protein is useful as a diagnostic marker for
CC prostatic carcinoma and B-cell cancers, possibly also for infertility,
CC and as a reagent for separating cancerous and non-cancerous cells.
CC The products may also be used to diagnose or treat Wolf-Hirschhorn
CC syndrome, associated with a deletion in the region of chromosome 4
CC (p16.3) where the zsig25 gene is located.
XX
SQ Sequence 1607 BP; 284 A; 540 C; 494 G; 289 T; 0 other;
Query Match 85.0%; Score 1563.4; DB 19; Length 1607;
Best Local Similarity 99.3%; Pred. No. 3.7e-300;
Matches 1570; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 260 GACCGCTGCGCGCGCGCTCCCGTCTGCTCGCGGTGATGAAACACCCACCGCGGC 319
DB 1 GAAATTCGGCTCGAGGGCGCTCCCGTCTGCTCGCGGTGATGAAACACCCACCGCGGC 60
QY 320 GCCCGCTGGGCAAGCCCTCTCGCTCTCTCTCGCCACTCTCGCGCGCGCGGCCAG 379
DB 61 GCGCGCTGGGCAAGGCCCTCTCGCTCTCTCTCGCCACTCTCGCGCGCGCGGCCAG 120
QY 380 CCTCTTGGGGAGAGTCCATCTCTTCCGCCAGAGCCCGGCCAAATACAGCATCACCCTTC 439
DB 121 CTTCTTGGGGAGAGTCCATCTCTTCCGCCAGAGCCCGGCCAAATACAGCATCACCCTTC 180
QY 440 ACGGGCAAGTGGAGCAGAGCGCTTCCCAAGCAGTACCCCTGTTCGCCCGCCCTGCG 499
DB 181 ACGGGCAAGTGGAGCAGAGCGCTTCCCAAGCAGTACCCCTGTTCGCCCGCCCTGCG 240
QY 500 CAGTGTCTTCGCTGCGTGGGGCGCGCATAGCTCCGACTACAGCATGTGGAGGAAGAAC 559
DB 241 CAGTGTCTTCGCTGCGTGGGGCGCGCATAGCTCCGACTACAGCATGTGGAGGAAGAAC 300
QY 560 CAGTGTCTCAGTAACGGGCTTCGCGACTTTTGGGAGCGCGCGGAGGCGCTGGGCGCTGATG 619
DB 301 CAGTGTCTCAGTAACGGGCTTCGCGACTTTTGGGAGCGCGCGGAGGCGCTGGGCGCTGATG 360
QY 620 AAGGAGATCAGAGCGCGGGAGGCGCTGCAGAGCGTGCACAGAGTGTTCGCGGCGCC 679
DB 361 AAGGAGATCAGAGCGCGGGAGGCGCTGCAGAGCGTGCACAGAGTGTTCGCGGCGCC 420
QY 680 GCGGTCCCGACCGCGGAGAGCTGCGCGGAGCTGGAGGTGACGCGCAGCGCACTCG 739
DB 421 GCGGTCCCGACCGCGGAGAGCTGCGCGGAGCTGGAGGTGACGCGCAGCGCACTCG 480
QY 740 CTGGTCTCGTTTGTGTGCGCATCTGCGCCAGCCCGACTGGTTCTGTGGCGTGGACAGC 799
DB 481 CTGGTCTCGTTTGTGTGCGCATCTGCGCCAGCCCGACTGGTTCTGTGGCGTGGACAGC 540
QY 800 CTGGACCTGTGCACGGGGACCGTTGGCGGGAACAGCGCGCGCTGGACCTGTACCCCTAC 859
DB 541 CTGGACCTGTGCACGGGGACCGTTGGCGGGAACAGCGCGCGCTGGACCTGTACCCCTAC 600
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Search completed: October 27, 2002, 08:12:45
Job time : 307 secs

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QY 860 GACGCGGGACGACAGCGGCTTACCTTCTCTCCCAACTTCGCCACCATCCCGCAG 919
DB 601 GACGCGGGACGACAGCGGCTTACCTTCTCTCCCAACTTCGCCACCATCCCGCAG 660
QY 920 GACACGCTGACCGAGATAAGCTCTCTCTCCAGGACACCCGCGCAACTCTTCTACTAC 979
DB 661 GACACGCTGACCGAGATAAGCTCTCTCTCCAGGACACCCGCGCAACTCTTCTACTAC 720
QY 980 CCGCGGCTGAAGGCCCTGCTCCATCGCCAGGCTGACACTGGTGGGCTGCGACAGAGC 1039
DB 721 CCGCGGCTGAAGGCCCTGCTCCATCGCCAGGCTGACACTGGTGGGCTGCGACAGAGC 780
QY 1040 CCCAGGCGCTTCATCCTCCCGCCAGTCTTCCAGCAGGAGGACATGATGTTAGAC 1099
DB 781 CCCAGGCGCTTCATCCTCCCGCCAGTCTTCCAGCAGGAGGACATGATGTTAGAC 840
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DB 841 AGCGCTCAGTTCAGAAACGCGCTGGACTGGAGGTCTTCCCTGTGGTCTCTTGGGA 900
QY 1160 CTGTGGGAGGCGACTGTGGAGGCTCGGACCAAGAGCAGGACTCGCTACGTCCGGGTC 1219
DB 901 CTGTGGGAGGCGACTGTGGAGGCTCGGACCAAGAGCAGGACTCGCTACGTCCGGGTC 960
QY 1220 CAGCGCGCCCAACACGCGGAGCCCTGCCCGAGCTCGAAGAAAGGCTGAGTGGTCCCT 1279
DB 961 CAGCGCGCCCAACACGCGGAGCCCTGCCCGAGCTCGAAGAAAGGCTGAGTGGTCCCT 1020
QY 1280 GATAACTGCGCTTAAGACACGAGCGCCCGAGCCCTGGGGCCCCCGAGGCCATGGGTG 1339
DB 1021 GATAACTGCGCTTAAGACACGAGCGCCCGAGCCCTGGGGCCCCCGAGGCCATGGGTG 1080
QY 1340 TCGGGGCGCTCTGTGCAGGCTCATGTGTGAGCGGCGAGGGCACAGGGGGTTTCGCGCT 1399
DB 1081 TCGGGGCGCTCTGTGCAGGCTCATGTGTGAGCGGCGAGGGCACAGGGGGTTTCGCGCT 1140
QY 1400 GCTCTCTACCGCGGTGAGCGCGCGGACCATCTCTGCACTGAGGGCCCTCTGGTGGCC 1459
DB 1141 GCTCTCTACCGCGGTGAGCGCGCGGACCATCTCTGCACTGAGGGCCCTCTGGTGGCC 1200
QY 1460 GGCACGGGCAATTGGGAAACAGCCCTCTCTTCCCACTTGTCTTAGGGGCCCCCGT 1519
DB 1201 GGCACGGGCAATTGGGAAACAGCCCTCTCTTCCCACTTGTCTTAGGGGCCCCCGT 1260
QY 1520 GTCCCGTCTCTCAGCCCTCTCTCTCGACGATAAAGTCAATCCCAAGGCTCCAGCT 1579
DB 1261 GTCCCGTCTCTCAGCCCTCTCTCTCGACGATAAAGTCAATCCCAAGGCTCCAGCT 1320
QY 1580 ACTCTAAATTTATCTCTCTTATAAGTTATTGCTGCTCCAGGAGATTGCTCTCATCGTCC 1639
DB 1321 ACTCTAAATTTATCTCTCTTATAAGTTATTGCTGCTCCAGGAGATTGCTCTCATCGTCC 1380
QY 1640 AGGGGCGTGGCTCCCGAGCGTGGTTCGACATACCTCAGACCTTGGTCTTAGGCTGTGCTGA 1699
DB 1381 AGGGGCGTGGCTCCCGAGCGTGGTTCGACATACCTCAGACCTTGGTCTTAGGCTGTGCTGA 1440
QY 1700 GCCCACTCTCCCGAGGGCGCATCCAGCGGGGCGCACTTGAGAGTGAATAAATAGGGCG 1759
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QY 1760 GTTTCGGAAGCGTCACTGTTTCCATGTTATGGATCTCTGCGCTTGAATAAAGACTATC 1819
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QY 1820 TCTGTTGCTCAAAAAA 1840
DB 1561 TCTGTTGATCAAAAAA 1581
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Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1692.4	92.0	1779	4	US-09-371-696-1	Sequence 1, Appli
2	1100.2	59.8	1105	2	US-08-799-173A-1	Sequence 1, Appli
3	343.8	18.7	400	1	US-08-644-326-1	Sequence 1, Appli
4	339	18.4	400	4	US-09-022-238-1	Sequence 1, Appli
5	304.8	16.6	506	2	US-08-799-173A-15	Sequence 15, Appli
6	204.2	11.1	316	2	US-08-799-173A-16	Sequence 16, Appli
7	204.2	11.1	316	2	US-08-799-173A-17	Sequence 17, Appli
8	71.6	3.9	4029	1	US-07-862-021B-9	Sequence 9, Appli
9	71.6	3.9	4029	1	US-08-313-288B-9	Sequence 9, Appli
10	71.6	3.9	4029	5	PCF-US93-03164-9	Sequence 9, Appli
11	62.2	3.4	3226	1	US-07-862-021B-11	Sequence 11, Appli
12	62.2	3.4	3226	1	US-08-313-288B-11	Sequence 11, Appli
13	62.2	3.4	3226	5	PCF-US93-03164-11	Sequence 11, Appli
14	57.6	3.1	1155	4	US-08-818-112-12	Sequence 12, Appli
15	57.6	3.1	1155	4	US-08-818-111-12	Sequence 12, Appli
16	57.6	3.1	1155	4	US-09-056-556-12	Sequence 12, Appli
17	57.2	3.1	1816	1	US-07-862-021B-13	Sequence 12, Appli
18	57.2	3.1	1816	1	US-08-313-288B-13	Sequence 13, Appli
19	57.2	3.1	1816	5	PCF-US93-03164-13	Sequence 13, Appli
20	55.4	3.0	1105	2	US-08-799-173A-1	Sequence 1, Appli
21	55	3.0	30001	1	US-08-125-468-1	Sequence 1, Appli
22	55	3.0	30001	2	US-08-474-933-1	Sequence 1, Appli
23	54.4	3.0	933	4	US-09-105-390-43	Sequence 43, Appli
24	54.4	3.0	1008	4	US-09-105-390-59	Sequence 59, Appli
25	54.4	3.0	2810	4	US-09-105-390-6	Sequence 6, Appli
26	52.4	2.8	1779	4	US-09-371-696-1	Sequence 1, Appli
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LOCATION: 19..1011
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 19..963
US-08-799-173A-1

Query Match 59.8%; Score 1100.2; DB 2; Length 1105;
Best Local Similarity 99.7%; Pred. NO. 1e-219;
Matches 1102; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 281 CCTGCTCTCTGCGGGTGTATGAAGAACCCAGCCGCGCGCCCTTGGGAGAGTCCATC 340
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QY 461 GCGTTCGCCAAGCAGTACCCCTGTTCGCGCCCTTGGGAGTGTCTGCTGTGGG 520
DB 181 GCGTTCGCCAAGCAGTACCCCTGTTCGCGCCCTTGGGAGTGTCTGCTGTGGG 240
QY 521 GCGGCGCATAGTCCGAGCTACAGCATGTGGAGGAAGAACCTAGTCAAGTAAAGGCGTG 580
DB 241 GCGGCGCATAGTCCGAGCTACAGCATGTGGAGGAAGAACCTAGTCAAGTAAAGGCGTG 300
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QY 641 GAGGCGCTGACAGAGCGTGACAGAGTGTTCGCGCGCGCGCGCTGCCAGCGGACCGGG 700
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QY 881 TTCACCTTCTCTCCCGCAACTTCGCCACCATCCGCGAGCACAGTGCACGAGATAAG 940
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QY 941 TCCTCTCTCTCCAGGACCCCGGCCAACTCTTCTACTACCCGCGGTGAAGCCCTGCT 1000
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QY 1001 CCATCGCCAGGGTGACACTGTGGGCTGTGCGACAGAGCCCGAGGCGCTTCATCCCTCC 1060
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QY 1061 GCCCAGTCTCTCCAGAGGACAAATGAGATTGTAGACAGCGCTCAGTTCCAGAAAG 1120
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QY 1121 CGCTGTGACTGTGAGGTCTCCCTGTGGTGTGGGACTGTGGGAGGCGCACTGTGG 1180
DB 841 CGCTGTGACTGTGAGGTCTCCCTGTGGTGTGGGACTGTGGGAGGCGCACTGTGG 900
QY 1181 AGGCTGGGACCAAGAGCAGGACTCGCTACGTCCGGGTCAGCGCGCGCCCAACAGCGGAG 1240
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QY 1361 CATGCTGAGGCGCGGAGGCGACA 1385
DB 1081 CATGCTGAGGCGCGGAGGCGACA 1105

RESULT 3

US-08-644-326-1
; Sequence 1, Application US/08644326
; Patent No. 5804382
; GENERAL INFORMATION:
; APPLICANT: Arthur J. Sytkowski and Meiheng Yang
; TITLE OF INVENTION: Methods for identifying Differentially Expressed Genes and
; TITLE OF INVENTION: Methods for identifying Differentially Expressed Genes and
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/644,326
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ralph A. Loren
; REGISTRATION NUMBER: 29,325
; REFERENCE/DOCKET NUMBER: NER-262
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 400 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-644-326-1

Query Match 18.7%; Score 343.8; DB 1; Length 400;
Best Local Similarity 97.0%; Pred. No. 5.4e-63;
Matches 393; Conservative 0; Mismatches 7; Indels 5; Gaps 4;

QY 850 GTACCCCTACGAGCGCGGAGGACAGCGGCTTCACCTTCTCTCCCACTTCGCCAC 909
DB 1 GTACCCCTACGAGCGCGGAGGAC-GACAGCGGCTTCACCTTCTCTCCCACTTCGCCAC 59
QY 910 CATCCGAGGACAGGCTGACCGAGATAGCTCCTCTCCAGCCACCGCCCACTC 969
DB 60 CATCCGAGGAC-GACAGGCTGACCGAGATAGCTCCTCTCTCCAGCCACCGCCCACTC 118
QY 970 CTTTACTACCGCGGCTGAAGGCCCTCGCTCCATCGCAGGCTGACACTGTGCGGCT 1029
DB 119 CTTTACTACCGCGGCTGAAGGCC--TGCTCCATCGCAGGCTGACACTGTGCGGCT 176
QY 1030 GCGACAGAGCCCGAGGCGCTTCATCCCTCCCGCCCGAGTCTGCCAGCAGGACATGA 1089
DB 177 GCGACAGAGCCCGAGGCGCTTCATCCCTCCCGCCCGAGTCTGCCAGCAGGACATGA 235

QY 1090 GATTGTAGACAGCGCTCAGTTCCAGAAACGGCGCTGGAGTGGAGGCTCTCCCTGTGGTC 1149
|||||
Db 236 GATTGTAGACAGCGCTCAGTTCCAGAAACGGCGCTGGAGTGGAGGCTCTCCCTGTGGTC 295
QY 1150 GTCTCTGGGACTGTGGAGGCGCACGTGTGGAGGCTCGGAGCAAGAGCAGGACTCGCTA 1209
|||||
Db 296 GTCTCTGGGACTGTGGAGGCGCACGTGTGGAGGCTCGGAGTCCAAGAGCAGGACTCCGTA 355
QY 1210 CGTCCGGGTCCAGCGCCGCAACAGCGGAGCCCTGCCCGGAGCT 1254
|||||
Db 356 CGCCCGGTCCAGCGCCGCAACAGCGGAGCCCTGCCCGGAGCT 400

RESULT 4

US-09-022-238-1
; Sequence 1, Application US/09022238
; Patent No. 6177244
; GENERAL INFORMATION:
; APPLICANT: Sytkowski, Arthur J. and Yang, Weiheng
; TITLE OF INVENTION: A novel NPG-1 Gene that is differentially expressed in prosta
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,238
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/644,326
; FILING DATE: 10-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Maravic-Magovcevic, Ivana
; REGISTRATION NUMBER: P-43,338
; REFERENCE/DOCKET NUMBER: NER-262CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 400 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..398

US-09-022-238-1
Query Match 18.4%; Score 339; DB 4; Length 400;
Best Local Similarity 96.3%; Pred. No. 5.3e-62;
Matches 390; Conservative 0; Mismatches 10; Indels 5; Gaps 4;

QY 850 GTACCCCTAGACGCGCGGACGACAGCGGTTACCTTCTCTCCCAACTTCGCCAC 909
|||||
Db 1 GTACCCCTAGACGCGGAC -GACAGCGGTTACCTTCTCTCCCAACTTCGCCAC 59
|||||

QY 910 CATCCCGGAGGACGCTGACGAGATACGTCCTCTCCAGCCGCCCAACTC 969
|||||
Db 60 CATCCCGCA -GACACGGTGACGAGATACGTCCTCTCCAGCCGCCCAACTC 118
|||||
QY 970 CTCTACTACCGCGGCTGAAGCGCCCTGCTCCCAATCGCCAGGTTGACACTGTTGGGCT 1029
|||||

Db 119 CTCTACTACCGCGGCTGAAGGCC--TGCTCCATCGCCAGGTTGACACTGTTGGCT 176
|||||
QY 1030 GGCACAGAGCCCGAGGCGCTTCATCCCTCCGCCCCAGTCTCCCGCAGGAGCAATGA 1089
|||||
Db 177 GGCACAGAGCCCGAGGCGCTTCATCCCTCCGCCCCAGTCTCCCGCAGCA -GGACAATGC 235
|||||
QY 1090 GATTGTAGACAGCGCTCAGTTCCAGAAACGGCGCTGGAGTGGAGGCTCTCCCTGTGGTC 1149
|||||
Db 236 GATTGTAGACAGCGCTCAGTTCCAGAAACGGCGCTGGAGTGGAGGCTCTCCCTGTGGTC 295
QY 1150 GTCTCTGGGACTGTGGAGGCGCACGTGTGGAGGCTCGGAGCAAGAGCAGGACTCGCTA 1209
|||||
Db 296 GTCTCTGGGACTGTGGAGGCGCACGTGTGGAGGCTCGGAGTCCAAGAGCAGGACTCCGTA 355
QY 1210 CGTCCGGGTCCAGCGCCGCAACAGCGGAGCCCTGCCCGGAGCT 1254
|||||
Db 356 CGCCCGGTCCAGCGCCGCAACAGCGGAGCCCTGCCCGGAGCT 400

RESULT 5

US-08-799-173A-15
; Sequence 15, Application US/08799173A
; Patent No. 5871969
; GENERAL INFORMATION:
; APPLICANT: HASTINGS, GREGG.
; APPLICANT: PATRICK J. DILLON
; TITLE OF INVENTION: HUMAN NEURONAL ATTACHMENT FACTOR-1
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/799,173A
; FILING DATE: 11-FEB-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF226
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 506 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-799-173A-15
Query Match 16.6%; Score 304.8; DB 2; Length 506;
Best Local Similarity 85.5%; Pred. No. 6.9e-55;
Matches 371; Conservative 0; Mismatches 59; Indels 4; Gaps 4;

QY 293 CGGGTGATGGAACCCAGCCGCGCGCTGGGAGGCCCTCTGCGCTCTCCTC 352
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Db 6 CGGCAGACGNNAAACCCAGCCGCGCTGCGCCCTGGGCAAGSCCTNCTGCGCTCTCCTC 65
|||||

QY 353 CTGGCCACTCTCGGCGCGCGCGCCAGCTCTTTGGGGAGAGTCCATCTGTTCCGCCAGA 412
|||||
Db 66 CTGGCCACTCTCGGCGCGCGC -ACCAGCCTCTTTGGGGAGAGTCCATCTNTTCCGCCAGA 124
|||||

QY 413 GCCCGGCGAAATACAGCATACCTTACGGGCAAGTGGAGCCAGCGGCTTCCCAAG 472
|||||
Db 125 GCCCGGCGAAATACAGCATACCTTACGGGCAAGTGGAGCCAGCGGCTTCCCAAG 184
QY 473 CAGTACCCCTGTTCGCGCCCTGCGCAGTGTCTTCCGCTGCGGCGCGCATAGC 532
|||||
Db 185 CAGTACCCCTGTTCGCGCCCTGCGCAGTGTCTTCCGCTGCGGCGCGCATAGC 243
QY 533 TCCGCTACAGCATGTGGAGGAAGAACACAGTACCTCAGTAAACGGGCTGCGCGACTTTGG 592
|||||
Db 244 TCCGCTACAGCATGTGGAGGAAGAACACAGTACCTCAGTAAACGGGCTGCGCGACTTTNG 303
QY 593 GAGCGCGGAGCGCTGGGCGCTGATGAAGAGATCGAGCGCGCGGAGGCGCTGCGAG 652
|||||
Db 304 GAGCGCGGAG-GCCTNGGCGTGTGATGAAGAGATCCGGGCGCGGAGGCGGTNCAAN 362
QY 653 AGCGTCACAGAGTGTTCGCGCGCGCGGCTGCGGCGCGGCGGCGGAGCGGCTGCGG 712
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Db 363 AGGTGCAAGAGTNTTTTCGGGCGCGG-GTTCGCGCGCGG-GTTCGCGCGCGGCGG 421
QY 713 GAGCTGAGGTGCA 726
|||||
Db 422 GNTTNNAGTTNA 435

RESULT 6

US-08-799-173A-16
; Sequence 16, Application US/08799173A
; Patent No. 5871969
; GENERAL INFORMATION:
; APPLICANT: HASTINGS, GREGG,
; APPLICANT: PATRICK J. DILLON
; TITLE OF INVENTION: HUMAN NEURONAL ATTACHMENT FACTOR-1
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/799,173A
; FILING DATE: 11-FEB-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF226
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 316 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-799-173A-16

Query Match 11.1%; Score 204.2; DB 2; Length 316;
Best Local Similarity 85.9%; Pred. No. 4.5e-34;
Matches 275; Conservative 0; Mismatches 38; Indels 7; Gaps 5;

QY 552 GGAAGAACACAGTACGTACAGCGGCTGCGGAGCTTTGCGAGCGCGGAGGCGCTGGG 611
|||
Db 1 GGCANNCCAGTACGTCA-TAACGGGCTGCGGAGCTTTGCGGA-NGCGGCGAGGCGCTGGG 58

QY 612 CGCTGATGAAGGAGATCGAGCGCGCGGAGCGGCTGCGAGAGCTGCACAGAGTGTTTT 671
|||||
Db 59 CGCTGATGAAGGAGATCAAGCGCGCGGAGCGGCTGCGAGAG-GTGACACAGGTGTTTT 117
QY 672 CGCGCGCGCGCTCCCGAGCGGCGGCGGAGCGAGCTGCGGCGGAGCTGGAGTGCAGCGCA 731
|||||
Db 118 CGCGCGCGG-GTNNCCAGGCNCCNGGCGAGAGCTCGGCGAACTGGNAGGTGCAGCGCA 176
QY 732 GGCACCTCGCTGCTCTGTTTGTGTTGCGGATCGTGCACGCCCGGACTGTTCTGTTGGCG 791
|||||
Db 177 GGCACCTCGCTGCTCTGTTTGTGTTGCGGATCGTGCACGCCCGGACTGTTCTGTTGGCG 236
QY 792 TGGACAGCCTTGGAGC---TGTGCGAGCGGAGCGGCTTGCGGCGGAAACAGGCGGCGCTGGACC 848
|||||
Db 237 TGGACAGCCTTGGAGCCTGTGANAACGGGAGCCTTTNGCGNAGNAACAGCGGCGGCTGGACC 296
QY 849 TGTACCCCTACGACGCGCGG 868
|||||
Db 297 TGTANCCCTAGGAGCGGCG 316

RESULT 7

US-08-799-173A-17
; Sequence 17, Application US/08799173A
; Patent No. 5871969
; GENERAL INFORMATION:
; APPLICANT: HASTINGS, GREGG,
; APPLICANT: PATRICK J. DILLON
; TITLE OF INVENTION: HUMAN NEURONAL ATTACHMENT FACTOR-1
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/799,173A
; FILING DATE: 11-FEB-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF226
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 316 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-799-173A-17

Query Match 11.1%; Score 204.2; DB 2; Length 316;
Best Local Similarity 85.9%; Pred. No. 4.5e-34;
Matches 275; Conservative 0; Mismatches 38; Indels 7; Gaps 5;

QY 552 GGAAGAACACAGTACGTACAGCGGCTGCGGAGCTTTGCGAGCGCGGAGGCGCTGGG 611
|||
Db 1 GGCANNCCAGTACGTCA-TAACGGGCTGCGGAGCTTTGCGGA-NGCGGCGAGGCGCTGGG 58
QY 612 CGCTGATGAAGGAGATCGAGCGCGGCGGAGCGGCTGCGAGAGCTGCACAGAGTGTTTT 671
|||||

Db 59 CGCTGATGAAGAGATCAAGAGCGGGGGGAGCGCTGCAGAG-GTGCACAGAGGTCTTTT 117
QY 672 CGGCGCCCGCTCCCGACGCGCACGGGCAGACGCTGGCGGAGCTGAGAGTGCAGCGCA 731
Db 118 CGGCGCCCG-GTNNCCAGCNCACNGGCAGACGCTGGCGAATCGGNAGGTGCAGCGCA 176
QY 732 GGCACCTCGCTGCTCTGTTTGTGTGCGCATCGTGCCCAAGCCCGACTGGTTTCGTGGGCG 791
Db 177 GGCACCTCGCTGCTCTGTTTGTGTGCGCATCGTGCCCAAGCCCGACTGGTTTCGTGGGCG 236
QY 792 TGCACAGCCTGCACC---TGTCCGAGGGGACCGTTGGCGGGAAACAGGGCGCTGGACC 848
Db 237 TGCACAGCCTGGAGCTGTGCANACGGGACCTTTNGCGNGNAACAGGCGNGTGGACC 296
QY 849 TGTACCCCTACGACGCGGG 868
Db 297 TGTANCCCTACGACGNGGG 316

RESULT 8

US-07-862-021B-9
; Sequence 9, Application US/07862021B
; Patent No. 5279966
; GENERAL INFORMATION:
; APPLICANT: Jessell, Thomas M
; APPLICANT: Klar, AviHu
; TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
; TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESS: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/862,021B
; FILING DATE: 19920405
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 40028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP U1
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4029 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 226...2647

US-07-862-021B-9

Query Match 3.9%; Score 71.6; DB 1; Length 4029;
Best Local Similarity 50.2%; Pred. No. 2.2e-06;
Matches 269; Conservative 0; Mismatches 249; Indels 18; Gaps 3;

QY 400 CTGTTCCGCGCAGCCCGCCCAATACAGCATCACCTTCACGGCGCAAGTGGAGCCAGAC 459
Db 819 CTGTCGCGCTCGGGAATGCCAAGTACAGACTCAGCTTTATGTGGAAGTGTGCGAGAA 878

QY 460 GGCCTTCCCAAGAGTACCCCTGTTCGCGCCCGCTGCGCAGTGTCTTCTGCTGCTGGG 519
Db 879 GACTCATCCAAAGGATTACCC-----TGTCTGGGCTAATCACTGTCTTGCCATCATTTGG 932
QY 520 GGCCTGGGATAGTCTCGGACTACAGCATGTGGAGGAGAACACAGTACGTACGTAAAGGGGT 579
Db 933 CGGATCCCACTCCAAAGAACTAGCTGCTGTGGGAGTACGGAGGGTATGCCAGTGAAGGGGT 992
QY 580 GGCCTGACTTTGGGAGCGCGGAGGCGCTGCGCTGATGAAGGAGATCGAGCGCGCGGG 639
Db 993 CAAGCAAGTTGCTGAACCTTGGCTCACCAGTAAATGAGGAGAGAAATTCGACACAGAG 1052
QY 640 GGAGGCGCTGCAGAGCGTGCACAGGT-----GTTTCGGCGCCCGCTGCCAG 690
Db 1053 TGATGAAGTCTCTCACTGTCATCAAGCCAAAGCCAGTGGCCATCTGCGCAGCTGTCAA 1112
QY 691 CGGACCGGGGAGAGCTGGCGGAGCTGGAGTGCAGCGCAGGCACTGCTGCTGCTCGTT 750
Db 1113 TGTGAGAGCAGCACCTTCAGCGGAAATCTCAGTGGAGCAGACACGCCACTTGTATGCTCTT 1172
QY 751 TGTGTTGGGCATCGTGCAGCCCGGAGTGTTCGTGGGCGTGGACAGCTTGACTGTG 810
Db 1173 CCTAACATGATGGCCCGGCTGCTGACTGGAACTGGGCTATCTGACAGAGATCTGTG 1232
QY 811 CGACGGGAGCCTTGGCGGGAACAG---GCGCGCTGGACCTGTACCCCTACGACGCGG 867
Db 1233 CACCAAGGAGTGTGGTGGTCCAGAAAGTGTGCAGGACCTAATTCCTGGGATGCTGG 1292
QY 868 GACGGACAGCGCTTCACCTTCTCTCCCACTTCGCCACCATCCCGCAGGACA 933
Db 1293 CACGGACAGCGGGTGCACCTAGAGTGCACAAACAGCCCAATTCCTTCAGGAAA 1348

RESULT 9

US-08-313-288B-9
; Sequence 9, Application US/08313288B
; Patent No. 5750502
; GENERAL INFORMATION:
; APPLICANT: Jessell, Thomas M. and AviHu Klar
; TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
; TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,288B
; FILING DATE: January 5, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 40028-A-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0526
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4029 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA


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;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 226...2647
US-08-313-288B-9

Query Match
Best Local Similarity 3.9%; Score 71.6; DB 1; Length 4029;
Matches 269; Conservative 0; Mismatches 249; Indels 18; Gaps 3;

QY 400 CTGTTCCGCGCAGAGCCCGCCCAATACAGCATCAGCTTCACGGGCAAGTGGAGCCAGAC 459
Db 819 CTGCTCGGCGCTGGGAACCTGCAAGTACAGACTCAGCTTTATGGAACTGGTCGGAGAA 878
QY 460 GGCTTTCCCAAGCAGTACCCCTGTTCGCGCCCGCCCTGCGCAGTGTTCGCTGCTGG 519
Db 879 GACTCATCCAAAGGATTACCC-----TCGTCGGGCTAATCACTGTCTGCCATCATTGG 932
QY 520 GGCGCGGCATAGCTCCGACTACAGATGTGGAGGAAGAACCCAGTACGTACGTAAACGGGT 579
Db 933 CGGATCCCACTCCAAAGAACTACGTGTCTGGGAGTACGGAGGATGCCAGTGAAGGGGT 992
QY 580 GCAGCGCTTCGCGAGCGCGGCGGAGCCCTGGCGCTCATCAAGGAGATCAGAGCGCGGG 639
Db 993 CAAGCAAGTGTGGAAGTGGCTTACCAAGTAAATAATGGAGGAAGAAATTCGACACAGAG 1052
QY 640 GGAGGCGCTCGAGAGCTGCAGAGGT-----GTTTTCGGCGCCCGCCCTGCCAG 690
Db 1053 TGATGAAGTCTCCTACATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1112
QY 691 CGCAGCGGCGAGAGCTCGCGGAGCTGGAGGTGCGAGCGAGCACTCGCTGTCTGCTT 750
Db 1113 TGTGAGAGCAGCACCCTCAGCCGAAATCTCAGTGGAGAGCAGCAGCAGCAGTGTGCT 1172
QY 751 TGTGTCGCGCATCGTCCCGAGCCCGCAGCTGGTTCGTCGGGCTGAGAGGATCGTGCAC 810
Db 1173 CCTAACCATGATGGGCGCCAGTCTCAGTGGAACTGGGCGCTATCTCGAGAGGATCTGTG 1232
QY 811 CGAGCGGCGAGCTGGCGGAGAACAG---GCGGCGCTGGAGCTGACCCCTACGACGCCGG 867
Db 1233 CACCAAGAGTGTGGCTGGGTCCAGAAAGTGTGCGAGGACCTAATTCCTGGGATCTGTG 1292
QY 868 GACGGACAGCGGCTTCACTTCTCTCCCTCCCAACTTCGCCCACTTCGCCGAGGACA 923
Db 1293 CACGGACAGCGGGGTGACCTACGAGTACCAAAACAGCCCAACAAATTCCTCAGGAAA 1348

RESULT 10
PCT-US93-03164-9
; Sequence 9, Application PC/TUS9303164
; GENERAL INFORMATION:
; APPLICANT: Jessell, Thomas M
; APPLICANT: Klar, Avihu
; TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
; TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/03164
; FILING DATE: 19930402
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

```

```

;
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 40028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 664-0550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4029 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 226...2647
PCT-US93-03164-9

Query Match
Best Local Similarity 3.9%; Score 71.6; DB 5; Length 4029;
Matches 269; Conservative 0; Mismatches 249; Indels 18; Gaps 3;

QY 400 CTGTTCCGCGCAGAGCCCGCCCAATACAGCATCAGCTTCACGGGCAAGTGGAGCCAGAC 459
Db 819 CTGCTCGGCGCTGGGAACCTGCAAGTACAGACTCAGCTTTATGGAACTGGTCGGAGAA 878
QY 460 GGCTTTCCCAAGCAGTACCCCTGTTCGCGCCCGCCCTGCGCAGTGTTCGCTGCTGG 519
Db 879 GACTCATCCAAAGGATTACCC-----TCGTCGGGCTAATCACTGTCTGCCATCATTGG 932
QY 520 GGCGCGGCATAGCTCCGACTACAGATGTGGAGGAAGAACCCAGTACGTACGTAAACGGGT 579
Db 933 CGGATCCCACTCCAAAGAACTACGTGTCTGGGAGTACGGAGGATGCCAGTGAAGGGGT 992
QY 580 GCAGCGCTTCGCGAGCGCGGCGGAGCCCTGGCGCTCATCAAGGAGATCAGAGCGCGGG 639
Db 993 CAAGCAAGTGTGGAAGTGGCTTACCAAGTAAATAATGGAGGAAGAAATTCGACACAGAG 1052
QY 640 GGAGGCGCTCGAGAGCTGCAGAGGT-----GTTTTCGGCGCCCGCCCTGCCAG 690
Db 1053 TGATGAAGTCTCCTACATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1112
QY 691 CGCAGCGGCGAGAGCTCGCGGAGCTGGAGGTGCGAGCGAGCACTCGCTGTCTGCTT 750
Db 1113 TGTGAGAGCAGCACCCTCAGCCGAAATCTCAGTGGAGAGCAGCAGCAGCAGTGTGCT 1172
QY 751 TGTGTCGCGCATCGTCCCGAGCCCGCAGCTGGTTCGTCGGGCTGAGAGGATCGTGCAC 810
Db 1173 CCTAACCATGATGGGCGCCAGTCTCAGTGGAACTGGGCGCTATCTCGAGAGGATCTGTG 1232
QY 811 CGAGCGGCGAGCTGGCGGAGAACAG---GCGGCGCTGGAGCTGACCCCTACGACGCCGG 867
Db 1233 CACCAAGAGTGTGGCTGGGTCCAGAAAGTGTGCGAGGACCTAATTCCTGGGATCTGTG 1292
QY 868 GACGGACAGCGGCTTCACTTCTCTCCCTCCCAACTTCGCCCACTTCGCCGAGGACA 923
Db 1293 CACGGACAGCGGGGTGACCTACGAGTACCAAAACAGCCCAACAAATTCCTCAGGAAA 1348

RESULT 11
US-07-862-021B-11
; Sequence 11, Application US/07862021B
; Patent No. 5279966
; GENERAL INFORMATION:
; APPLICANT: Jessell, Thomas M
; APPLICANT: Klar, Avihu
; TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
; TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:

```

ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/862,021B
FILING DATE: 19920405
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40028
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 3226 base pairs
TYPE: NUCLEIC ACID
STRAINEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 136..2543
US-07-862-021B-11

Query Match 3.4%; Score 62.2; DB 1; Length 3226;
Best Local Similarity 49.0%; Pred. No. 0.00019;
Matches 265; Conservative 0; Mismatches 258; Indels 18; Gaps 3;

QY 401 TGTTCGCCAGAGCCCGGCAATACAGCATCACCTTCACGGGCAAGTGGAGCCAGACG 460
DB 715 TGTCTGCTGCTGGAACTGCCAAATACAGCTAAGCTTTATGGAATTTGGTCGGAATA 774
QY 461 GCCTTCCCAAGCAGTACCCCTGTTCCGCCCCCTCGCAGTGTCTTCGCTGCTGGGG 520
DB 775 ACACATCCCAAGACTTTCC-----TCGGCGCACCAACCATTTGGTCTCGCATTTGTT 828
QY 521 GCGCGCATAGTCCGACTACAGCATGTGGAGGAAGAACAGTACGTACGTACACGGCTG 580
DB 829 AGCTCTCACTAAAGAACTACATCTTTGGGAGTATGGAGGTTATGCTAGTGAAGGTGC 888
QY 581 CGCGACTTTTCGGAGCGCGGAGGCTGGCGCTGATGAAGGAGATCGAGCGCGGGG 640
DB 889 AAGCAGTTGTCAGAGCTGGGATCCCCAGTCAAGATGAAGAGAAATTCACACAAAGT 948
QY 641 GAGGCGCTGCAGAGCGTGCACGAGG-----TGTTTTTCGGCGCCCGCTGCCACG 691
DB 949 GATGAGGTTTAACTAGTCAAGGCAAAAGCACAGTGCCTGCGTGGCAGCTCTGAAT 1008
QY 692 GGCACCGGCGAGCTGCGGGAGCTGGAGTGCACGCGGAGGACTGCGTGTCTGCTGTT 751
DB 1009 GTGAGAGCTGCTCCCTCTGCTGAGTTTCTGTTGATGCGACCGGACCTGATGCTCTTC 1068
QY 752 GTGGTGGCATCTGTGCCACCGCCGACTGTTGCTGGGCGTGACAGCTGGACCTGTGTC 811
DB 1069 CTCACCATCTGTTGGGCGGAGTCCGACTGATGAGGCTGCTGCTGAGGACCTCTGC 1128
QY 812 GACGGGACGTTGGCGGAACAG---GCGGCGCTGGAGCTGTACCCCTACGACGCGCGG 868
DB 1129 ACCAAGAGCTGTGGCTGAGTTTACAGAAAGTGTGACAGATTTAATCCCTGGGATGCGGC 1188
QY 869 ACGGACGCGGCTTACCTTCTCCTCCCACTTCGCCCACTCCGCGAGGACGCGGTG 928

DB 1189 ACAGACAGTGGCGTCACTATGATGATCACCACCAAAACCTACAGTTCTCTCAAGAGAATT 1248
QY 929 A 929
DB 1249 A 1249
RESULT 12
US-08-313-288B-11
Sequence 11, Application US/08313288B
Patent No. 5750502
GENERAL INFORMATION:
APPLICANT: Jessell, Thomas M. and Avihu Klar
TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,288B
FILING DATE: January 5, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40028-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 3226 base pairs
TYPE: nucleic acid
STRAINEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 136..2543
US-08-313-288B-11

Query Match 3.4%; Score 62.2; DB 1; Length 3226;
Best Local Similarity 49.0%; Pred. No. 0.00019;
Matches 265; Conservative 0; Mismatches 258; Indels 18; Gaps 3;

QY 401 TGTTCGCCAGAGCCCGGCAATACAGCATCACCTTCACGGGCAAGTGGAGCCAGACG 460
DB 715 TGTCTGCTGCTGGAACTGCCAAATACAGCTAAGCTTTATGGAATTTGGTCGGAATA 774
QY 461 GCCTTCCCAAGCAGTACCCCTGTTCCGCCCCCTCGCAGTGTCTTCGCTGCTGGGG 520
DB 775 ACACATCCCAAGACTTTCC-----TCGGCGCACCAACCATTTGGTCTCGCATTTGTT 828
QY 521 GCGCGCATAGTCCGACTACAGCATGTGGAGGAAGAACAGTACGTACGTACACGGCTG 580
DB 829 AGCTCTCACTAAAGAACTACATCTTTGGGAGTATGGAGGTTATGCTAGTGAAGGTGC 888
QY 581 CGCGACTTTTCGGAGCGCGGAGGCTGGCGCTGATGAAGGAGATCGAGCGCGGGG 640
DB 889 AAGCAGTTGTCAGAGCTGGGATCCCCAGTCAAGATGAAGAGAAATTCACACAAAGT 948
QY 641 GAGGCGCTGCAGAGCGTGCACGAGG-----TGTTTTTCGGCGCCCGCTGCCACG 691

Db 949 GATGAGTTTAAACAGTCATCAAGGCAAAAGCACAGCTGGCTGCCTGGCAGCCTCTGAAT 1008
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Db 1009 GTGAGAGCTGCTCCCTCTCTGCTGAGTTTCTGTGTATCGCGCACCGCACTGATGCTCTTC 1068
QY 752 GTGGTGGCATGTCGCCAGCCCGCACTGGTTCTGTGGGCTGGACAGCCTGGACCTGTGC 811
Db 1069 CTCACCATGCTGGGGCCAGTCCGAGTGAATGTGGGCTGTCTGCTGAGGACCTCTGC 1128
QY 812 GACGGGAGCGTTGGCGGGAACAG---GCGGCGCTGGACCTGTACCCCTACGACGCCGG 868
Db 1129 ACCAAGGACTGTGGTGGGTTTCAGAAAGTCTGTCAGAGATTAAATCCCTGGGATGCCGC 1188
QY 869 AGGAGAGCGGCTTCACTTCTCCCTCCCACTTCGCCACCATCCCGCAGGACGGTG 928
Db 1189 ACAGAGTGGGCTACCTATGAGTCACCCCAACACCTACAGTTCCTCAAGAGAAGATT 1248
QY 929 A 929
Db 1249 A 1249

RESULT 13

PCT-US93-03164-11
; Sequence 11, Application PC/TUS9303164
; GENERAL INFORMATION:
; APPLICANT: Jessell, Thomas M
; APPLICANT: Klar, Avihu
; TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
; TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/03164
; FILING DATE: 19930402
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 40028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3226 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 136...2543
PCT-US93-03164-11

Query Match 3.4%; Score 62.2; DB 5; Length 3226;

Best Local Similarity 49.0%; Pred. No. 0.00019;
Matches 265; Conservative 0; Mismatches 258; Indels 18; Gaps 3;
QY 401 TGTTCGCCAGAGCCCGCGCCAAATACAGATCACCTTACAGGGCAAGTGGAGCCAGACG 460
Db 715 TGTCTGCTGCTGGAACTCCCAATACAGGCTAACCTTTTATGGAATTTGGTCGGAATA 774
QY 461 GCCTTCCCAAGCAGTACCCCTGTTCGCCGCCCTGCGCAGTGGTCTTCGCTGCTGGGG 520
Db 775 ACACATCCCAAGACATTTC-----TCGGGCGACCAACATTTGGTCTGGATCATGGT 828
QY 521 GCGGCGCATAGTCCGATACAGCATGTGGAGGAAGAACACAGTACGTACGTAACGGCTG 580
Db 829 AGCTCTCACTCAAGAACTACATCCCTTTGGAGTATGGAGGTATGCTAGTGAAGGTGC 888
QY 581 CGCGACTTTTCGGAGCGCGGAGGCTGGGCGCTGATGAAGGAGATCGAGGCGCGGGG 640
Db 889 AAGCAGGTTTCAGAGAGCTGGGATCCCGCAGTCAAGATGAAGAAGAAATCGACAACAAGT 948
QY 641 GAGGCGCTGCAGAGCTGCACGAGG-----TGTTCGGCGCGCGCGCTCCCGCAGC 691
Db 949 GATGAGTTTAAACAGTCATCAAGGCAAAAGCACAGTGGCTGCCTGGCAGCCTCTGAAT 1008
QY 692 GGCACGGGCGACGCTCGCGGAGCTGGAGTGCAGCGCAGGCACTCGTGGTCTGTTT 751
Db 1009 GTGAGAGCTGCTCCCTCTCTGCTGAGTTTCTGTGTATCGCGCACCGCACTGATGCTCTTC 1068
QY 752 GTGGTGGCATGTCGCCAGCCCGCACTGGTTCTGTGGGCTGGACAGCCTGGACCTGTGC 811
Db 1069 CTCACCATGCTGGGGCCAGTCCGAGTGAATGTGGGCTGTCTGCTGAGGACCTCTGC 1128
QY 812 GACGGGAGCGTTGGCGGGAACAG---GCGGCGCTGGACCTGTACCCCTACGACGCCGG 868
Db 1129 ACCAAGACTGTGGTGGGTTTCAGAAAGTCTGTCAGAGATTAAATCCCTGGGATGCCGC 1188
QY 869 ACGGACAGCGCTTCACTTCTCCCTCCCACTTCGCCACCATCCCGCAGGACACGGTG 928
Db 1189 ACAGACAGTGGGCTACCTATGAGTCACCCCAACACCTACAGTTCCTCAAGAGAAGATT 1248
QY 929 A 929
Db 1249 A 1249
RESULT 14
US-08-818-112-12
; Sequence 12, Application US/08818112
; Patent No. 6290969
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Houghton, Raymond
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Twardzik, Daniel R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/818,112

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;
; FILING DATE: 13-MAR-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.411C6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1155 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-818-112-12

Query Match          3.1%; Score 57.6; DB 4; Length 1155;
Best Local Similarity 43.9%; Pred. No. 0.0014;
Matches 246; Conservative 0; Mismatches 314; Indels 0; Gaps 0;

QY 335 GCCTCTGGGCTCTCTCTCTGGCCACTCTCGGGCGCGCGCCAGCCTCTTGGGGGAGAG 394
Db 141 GCCACCGGAGCTACCCGGCTCAAGGTCACCGTGCAGGGGTGCTCCAAGGGTGGCC 200
QY 395 TCCATCTGTTCCGCCAGAGCCCGGCCAATACAGCATCACCTTCAAGGGCAAGTGGAGC 454
Db 201 GCGAGCGCGCATCCACACCGAGTTCAACAGACGATCGCGCGACCGCGGCTCTCC 260
QY 455 CAGACGGCTTCCCAAGAGTACCCCTGTTCGGCGCCCGCTGCGCAGTGGTTCGCTG 514
Db 261 TCGACCAACCACTTCCGAGATCCCGGATCCCGACGACGCGCGCGGGGATCCGG 320
QY 515 CTGGGGCGCGCATAGCTCCGACTACAGCATGTGGAGGAAGAACAGTACGTACGTAAC 574
Db 321 GACCGCTTGTGTCGGGACCGTTACGCCGAGTTGATACGCCGCTACAGCCAGATC 380
QY 575 GTGCGCATCGTCCCGAGCCCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 634
Db 381 GAGATCGGATCATGGGCACTGTCCGGGAGGAGGCTCATCGAGCGTTCAACACC 440
QY 635 GCGGGGAGGCGCTGCAGAGCGTGCAGAGGTGTTTCGGCGCCCGCCCGTCCCGAGCG 694
Db 441 GGGGAGGACCTGTATTCGTTCCGCGTCCCGGGTTCGCGTGCACGAGGTC 500
QY 695 ACCGGGCGAGCGTCGGCGGAGCTGGAGGTGCAGCGCAGGCACTCGCTGCTCTGTTTG 754
Db 501 ACCGGGAGTTTGGGCGCGGGTCAAGGCGATGTCTACGGGCTGTTTACGGGTTGAGC 560
QY 755 GTGCGCATCGTCCCGAGCCCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 814
Db 561 GCCTACGGCTGTGCGAGCAGTTGAAATCTCCACCGAGGAAGCCAAACAGCAGATGAC 620
QY 815 GGGGACGTTGGGGGAACAGCGGGCGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 874
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QY 875 AGCGGCTTCACCTTCCTC 894
Db 681 CGCAAGCGGCTACACCTC 700

RESULT 15
US-08-818-111-12
; Sequence 12, Application US/08818111
; Patent No. 633852
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, David C.
; APPLICANT: Campos-Neto, Antonia
; APPLICANT: Houghton, Raymond
; APPLICANT: Vedvick, Thomas S.
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QY 875 AGCGCTTCACCTTCCTC 894
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Db 681 CGCAGGACGGCTACACCTC 700

Search completed: October 27, 2002, 11:16:08
Job time : 101 secs

